

OM protein - protein search, using sw model  
 Run on: August 29, 2007, 08:45:19 ; Search time 271 Seconds  
 (without alignments)  
 1079.784 Million cell updates/sec

Title: US-09-943-780-69  
 Perfect score: 3135  
 Sequence: 1 MCSRVPLLLPLLLLALGPG.....PLMGFFGPGQLQSLHAKPYI 598  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 2782304 seqs, 48933398 residues  
 Total number of hits satisfying chosen parameters: 2782304  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%

Database : A.Geneseq 200701:.\*  
 Listing first 1500 summaries  
 1: geneseqp1980s:.\*  
 2: geneseqp1990s:.\*  
 3: geneseqp2000s:.\*  
 4: geneseqp2001s:.\*  
 5: geneseqp2002s:.\*  
 6: geneseqp2003as:.\*  
 7: geneseqp2003bs:.\*  
 8: geneseqp2004s:.\*  
 11: geneseqp2007s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY06484	standard; protein; 598 AA.				
DE	Human tumour-associated protein PRO357.					
PN	WO9935170-A2.					
PD	15-JUL-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 2;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;				
RESULT 2						
ID	AAB01322	standard; protein; 598 AA.				
DE	Human PRO357 polypeptide.					
PN	WO200032776-A2.					
PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;				
RESULT 3						
ID	AAY93691	standard; protein; 598 AA.				
DE	Amino acid sequence of novel polypeptide PRO357.					
PN	WO200037640-A2.					
PD	29-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;				
RESULT 4						
ID	AAU83643	standard; protein; 598 AA.				
DE	Human PRO protein, Seq ID No 104.					
PN	WO2000208288-A2.					
PD	31-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;				
RESULT 5						
ID	ADY31844	standard; protein; 598 AA.				
DE	Novel human secreted and transmembrane protein PRO357.					
PN	WO200193983-A1.					
PD	13-DEC-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 5;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;				
RESULT 6						
ID	ABU55931	standard; protein; 598 AA.				

DE Human secreted/transmembrane protein PRO357.  
 PN US2002142959-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 7  
 ID ABU80790 standard; protein; 598 AA.  
 DE Human PRO polypeptide #52.  
 PN US2003036635-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 8  
 ID ABO33756 standard; protein; 598 AA.  
 DE Novel human secreted and transmembrane protein PRO357.  
 PN US2003045687-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 9  
 ID ABU60241 standard; protein; 598 AA.  
 DE Human PRO polypeptide #12.  
 PN US2002132768-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 10  
 ID ABU64927 standard; protein; 598 AA.  
 DE Human secreted/transmembrane protein PRO357.  
 PN US2002173463-A1.  
 PD 21-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 11  
 ID ABU58361 standard; protein; 598 AA.  
 DE Novel human secreted protein PRO357.  
 PN US2002150976-A1.  
 PD 17-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 12  
 ID ABU57247 standard; protein; 598 AA.  
 DE Human PRO357 protein.  
 PN US2002142958-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 13  
 ID ABU56312 standard; protein; 598 AA.  
 DE Human secreted/transmembrane protein, PRO357.  
 PN US2002132981-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 14  
 ID ABU60352 standard; protein; 598 AA.  
 DE Novel human secreted and transmembrane protein PRO357.  
 PN US2002168715-A1.  
 PD 14-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3135; DB 6; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
 RESULT 15  
 ID ABU82099 standard; protein; 598 AA.  
 DE Novel human secreted and transmembrane protein PRO357.

PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 16  
ID ABU11313 standard; protein; 598 AA.  
DE Human pro357 protein sequence.  
PN US2002127643-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 17  
ID ABU67132 standard; protein; 598 AA.  
DE Human PRO polypeptide #12.  
PN US2002165143-A1.  
PD 07-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 18  
ID ABJ72279 standard; protein; 598 AA.  
DE Human PRO357 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 19  
ID ABJ72407 standard; protein; 598 AA.  
DE Human PRO357 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 20  
ID ABO34302 standard; protein; 598 AA.  
DE Human secreted/transmembrane polypeptide PRO 357.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 21  
ID ABJ72109 standard; protein; 598 AA.  
DE Human membrane bound receptor/protein PRO357 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 22  
ID ADB83594 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 23  
ID ADB80700 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 24  
ID ADB73241 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096968-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 25  
ID ADB78323 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 26  
ID ADB84971 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 27  
ID ADB78077 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 28  
ID ADB87143 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 29  
ID ADB84725 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 30  
ID ADB83840 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 31  
ID ADB72995 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 32  
ID ADC25825 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2002142419-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 33  
ID ADC25583 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2002156004-A1.  
PD 24-OCT-2002.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 34  
ID ADC25704 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003077698-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 35  
ID ADC36833 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US200308065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 36  
ID ADC21823 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 37  
ID ADC49854 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 38  
ID ADC49053 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 39  
ID ADC49570 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 40  
ID ADC47431 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 41  
ID ADC47176 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 42  
ID ADC78051 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 43  
ID ADD06286 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 44  
ID ADC77805 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 45  
ID ADD50768 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 46  
ID ADD51014 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 47  
ID ADD50495 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 48  
ID ADD50249 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 49  
ID ADD51260 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 50  
ID ADH27489 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003083479-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 51  
ID ADC48807 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;

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Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 56
ID ADD85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 57
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US200309362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 61
ID ADD73561 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 70
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
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ID ADD85535 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 71  
ID ADE05084 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 72  
ID ADD75297 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 73  
ID ADD76841 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 74  
ID ADD86609 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 75  
ID ADD78077 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 76  
ID ADE71538 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003096742-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 77  
ID ADD77595 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 78  
ID ADD77831 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 79  
ID ADD85289 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 80  
ID ADD73821 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 81  
ID ADD74559 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 82  
ID ADD77087 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 83  
ID ADD85781 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 84  
ID ADE05330 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 85  
ID ADD74805 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 86  
ID ADG05617 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 87  
ID ADG27171 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 88  
ID ADG11234 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.

PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 89  
ID ADG12013 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 90  
ID ADF94570 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 91  
ID ADG6666 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 92  
ID ADG63481 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003211570-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 93  
ID ADH39010 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 94  
ID ADH43210 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003207401-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 95  
ID ADG34100 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 96  
ID ADI33570 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 97  
ID ADH69664 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2004019183-A1.

PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 98  
ID ADI29825 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 99  
ID ADM27222 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 100  
ID ADK66580 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 101  
ID ADN00448 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2004091972-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 102  
ID ADU25372 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2004220385-A1.  
PD 04-NOV-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 103  
ID ADY39535 standard; protein; 598 AA.  
DE Human insulin-like growth factor homolog PRO357 precursor protein.  
PN US2005048613-A1.  
PD 03-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 9; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 104  
ID ADY73816 standard; protein; 598 AA.  
DE Human PRO357 protein, SEQ ID NO: 69.  
PN US2005059115-A1.  
PD 17-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 9; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 105  
ID AEG19662 standard; protein; 598 AA.  
DE Human secreted protein PRO357.  
PN WO2006026222-A2.  
PD 09-MAR-2006.  
PA (GETH ) GENENTECH INC.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 106  
ID AEH50165 standard; protein; 598 AA.  
DE Human CDNA clone DNA44804-1248 protein product PRO357 SEQ ID NO: 69.  
PN US2006105427-A1.

PD 18-MAY-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 107  
ID AEH49290 standard; protein; 598 AA.  
DE Human secreted polypeptide PRO357, SEQ ID NO:104.  
PN EPI659177-A2.  
PD 24-MAY-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 108  
ID AEI36373 standard; protein; 598 AA.  
DE Human PRO protein amino acid sequence - SEQ ID 69.  
PN US2006127983-A1.  
PD 15-JUN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 109  
ID AEK48325 standard; protein; 598 AA.  
DE Human PRO357 amino acid sequence.  
PN EPI686174-A1.  
PD 02-AUG-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 110  
ID AEK62918 standard; protein; 598 AA.  
DE Human PRO357 polypeptide, SEQ ID NO: 104.  
PN EPI700867-A2.  
PD 13-SEP-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 111  
ID AEL16958 standard; protein; 598 AA.  
DE Human secreted polypeptide PRO357, SEQ ID NO:104.  
PN EPI702928-A2.  
PD 20-SEP-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 10; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.3e-190;  
RESULT 112  
ID AAY17831 standard; protein; 598 AA.  
DE Human PRO357 protein sequence.  
PN WO9928462-A2.  
PD 10-JUN-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 3126; DB 2; Length 598;  
Best Local Similarity 99.8%; Pred. No. 1.6e-189;  
RESULT 113  
ID AAB07428 standard; protein; 673 AA.  
DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).  
PN WO200042170-A1.  
PD 20-JUL-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 98.4%; Score 3083.5; DB 3; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 114  
ID AAB87533 standard; protein; 673 AA.  
DE Human PRO1282.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 4; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 115  
ID AAB65166 standard; protein; 673 AA.  
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.  
PN WO200073454-A1.  
PD 07-DEC-2000.

PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 4; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 116  
ID AAU75266 standard; protein; 673 AA.  
DE Human Slit-like protein #1.  
PN WO200212346-A2.  
PD 14-FEB-2002.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 117  
ID ABG95858 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 118  
ID ABG78042 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein (LRSG-1).  
PN US2002072089-A1.  
PD 13-JUN-2002.  
PA (HOLT) HOLTZMAN D A.  
PA (MACB) MCCARTHY S A.  
PA (BUSE) BUSFIELD S J.  
PA (PANY) PAN Y.  
PA (WHIT) WHITE D.  
PA (KHOD) KHODADOUST M M.  
PA (GUWW) GU W.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 119  
ID ABUS7981 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 120  
ID ABUS9059 standard; protein; 673 AA.  
DE Novel human secreted or transmembrane protein PRO1282.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 121  
ID ABUS2571 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 122  
ID ABUS60490 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, #19.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 123  
ID ABUI3872 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 124

ID ABU72457 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003003531-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 125  
 ID ABU90883 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003018173-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 126  
 ID ABO33942 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003009013-A1.  
 PD 09-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 127  
 ID ABO33942 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003009013-A1.  
 PD 09-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 128  
 ID ABU71513 standard; protein; 673 AA.  
 DE Human secreted polypeptide PRO1282.  
 PN US2003013855-A1.  
 PD 16-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 129  
 ID ABU72294 standard; protein; 673 AA.  
 DE Human PRO polypeptide #8.  
 PN US2002182638-A1.  
 PD 05-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 130  
 ID ABU90967 standard; protein; 673 AA.  
 DE Human PRO polypeptide #8.  
 PN US2003018168-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 131  
 ID ABU5206 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein, #19.  
 PN US2003027162-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 132  
 ID ABO25903 standard; protein; 673 AA.  
 DE Human PRO1282 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 133  
 ID ABO27288 standard; protein; 673 AA.  
 DE Human secreted/transmembrane polypeptide PRO1282.

PN US2003009012-A1.  
 PD 09-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 134  
 ID ABU92483 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003045684-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 135  
 ID ABU81153 standard; protein; 673 AA.  
 DE Human secreted polypeptide PRO1282.  
 PN US2003027212-A1.  
 PD 08-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 136  
 ID ABO53268 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003027986-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 137  
 ID ABU58912 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein, #19.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 138  
 ID ABU92290 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003022187-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 139  
 ID ABU59355 standard; protein; 673 AA.  
 DE Novel human secreted or transmembrane protein PRO1282.  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 140  
 ID ABU98270 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2002183493-A1.  
 PD 05-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 141  
 ID ABU89275 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003036634-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 142  
 ID ABU82482 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2002183494-A1.  
 PD 05-DEC-2002.  
 PA (GETH ) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 143  
 ID ABU92121 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003017476-A1.  
 PD 23-JAN-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 144  
 ID ABU96446 standard; protein; 673 AA.  
 DE Human PRO polypeptide #8.  
 PN US2003027993-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 145  
 ID ABU10827 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2002123463-A1.  
 PD 05-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 146  
 ID ABU1579 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2002177164-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 147  
 ID ABU72116 standard; protein; 673 AA.  
 DE Human PRO polypeptide #8.  
 PN US2003023042-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 148  
 ID ABU88518 standard; protein; 673 AA.  
 DE Human secreted and transmembrane polypeptide PRO1282.  
 PN US2002197615-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 149  
 ID ABO34032 standard; protein; 673 AA.  
 DE Human PRO1282 polypeptide.  
 PN US2003017981-A1.  
 PD 23-JAN-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 150  
 ID ADB17073 standard; protein; 673 AA.  
 DE Human transmembrane PRO polypeptide (SeqID 16).  
 PN US2003050462-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 151  
 ID ADA37563 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003008297-A1.  
 PD 09-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 152

ID ADA21249 standard; protein; 673 AA.  
 DE Human secreted/transmembrane polypeptide PRO1282.  
 PN US2003054404-A1.  
 PD 20-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 153  
 ID ABO44246 standard; protein; 673 AA.  
 DE Human secreted/transmembrane polypeptide PRO 1282.  
 PN US2003018172-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 154  
 ID ADA10036 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein, PRO1282.  
 PN US2003059831-A1.  
 PD 27-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 155  
 ID ADA19878 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003069394-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 156  
 ID ADB17261 standard; protein; 673 AA.  
 DE Human transmembrane PRO polypeptide (SeqID 16).  
 PN US2003050465-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 157  
 ID ADA17580 standard; protein; 673 AA.  
 DE Human PRO1282 polypeptide.  
 PN US2003054987-A1.  
 PD 20-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 158  
 ID ADA27688 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003054359-A1.  
 PD 20-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 159  
 ID ADA20050 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003055222-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 160  
 ID ABO34174 standard; protein; 673 AA.  
 DE Human secreted/transmembrane polypeptide PRO 1282.  
 PN US2003060601-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 161  
 ID ADA94268 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003059832-A1.  
 PD 27-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;

Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 162  
ID ADA38493 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 163  
ID ADA92614 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 164  
ID ADA00347 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 165  
ID ABO53118 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 166  
ID ADA22175 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO1282.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 167  
ID ABO22488 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 168  
ID ADA06341 standard; protein; 673 AA.  
DE Human secreted/transmembrane PRO polypeptide #13.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 169  
ID ADA39034 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 170  
ID ADB8589 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 171  
ID ADB96060 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 172  
ID ADB68268 standard; protein; 673 AA.  
DE Human PRO1282 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 173  
ID ADB68075 standard; protein; 673 AA.  
DE Human PRO1282 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 174  
ID ADB90892 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 175  
ID ADC57532 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 176  
ID ADC54896 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 177  
ID ADC11763 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 178  
ID ADC06972 standard; protein; 673 AA.  
DE Human PRO1282 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 179  
ID ADC56185 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 180  
ID ADC17151 standard; protein; 673 AA.  
DE Mammalian PRO polypeptide (SeqID 16).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 181  
ID ADC07240 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003068647-A1.  
PD 10-APR-2003.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 182  
 ID ADC11230 standard; protein; 673 AA.  
 DE Human secreted/transmembrane protein PRO1282.  
 PN US2003069403-A1.  
 PD 10-APR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 183  
 ID ADC14849 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003073208-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 184  
 ID ADC2344 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003138882-A1.  
 PD 24-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 185  
 ID ADC14352 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003082546-A1.  
 PD 01-MAY-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 186  
 ID ADD07894 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003068623-A1.  
 PD 10-APR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 187  
 ID ADC81709 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2003083461-A1.  
 PD 01-MAY-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 188  
 ID ADD07351 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2002193299-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 189  
 ID ADC82242 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2003059833-A1.  
 PD 27-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 190  
 ID ADD08422 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003073090-A1.  
 PD 17-APR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 191  
 ID ADD06671 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2002193300-A1.  
 PD 19-DEC-2002.

PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 192  
 ID ADC82918 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2003059783-A1.  
 PD 27-MAR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 193  
 ID ADD55025 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2003077593-A1.  
 PD 24-APR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 194  
 ID ADD36020 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003105298-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 195  
 ID ADD5983 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2003077594-A1.  
 PD 24-APR-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 196  
 ID ADD54421 standard; protein; 673 AA.  
 DE Human PRO polypeptide #13.  
 PN US2002132253-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 197  
 ID ADE26575 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003087304-A1.  
 PD 08-MAY-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 198  
 ID ADE26042 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003087305-A1.  
 PD 08-MAY-2003.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 199  
 ID ADF66979 standard; protein; 673 AA.  
 DE Human PRO1282 amino acid sequence SEQ ID NO:52.  
 PN US2002198148-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 200  
 ID ADG01021 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.  
 PN US2003078387-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
 RESULT 201  
 ID ADG08574 standard; protein; 673 AA.  
 DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 202  
ID ADH37584 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 203  
ID ADH24048 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 204  
ID ADH34074 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 205  
ID ADH29907 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 206  
ID ADH21878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 207  
ID ADH85282 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 208  
ID ADH24558 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 209  
ID ADH37414 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 210  
ID ADH02003 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180837-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 211  
ID ADH37584 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 212  
ID ADH85622 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 213  
ID ADH24218 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 214  
ID ADH38512 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 215  
ID ADH83633 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 216  
ID ADH29441 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 217  
ID ADH27557 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 218  
ID ADH37754 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 219  
ID ADH37931 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181649-A1.  
PD 25-SEP-2003.



PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 220  
ID ADH57351 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 221  
ID ADH53493 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 222  
ID ADH53663 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 223  
ID ADH51999 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 224  
ID ADH49854 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 225  
ID ADI25364 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 226  
ID ADH90157 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 227  
ID ADI25534 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 228  
ID ADH97708 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 229  
ID ADI35233 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 230  
ID ADI03556 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 231  
ID ADI11913 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 232  
ID ADH89987 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 233  
ID ADH99725 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 234  
ID ADH98388 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 235  
ID ADI11063 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 236  
ID ADI11573 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 237  
ID ADH98218 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 238  
ID ADH97708 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

ID ADH98558 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 239  
ID ADH98048 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 240  
ID ADI05036 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 241  
ID ADI03386 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 242  
ID ADI04781 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 243  
ID ADH78235 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 244  
ID ADI19579 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 245  
ID ADH90327 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 246  
ID ADI03046 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 247  
ID ADH77895 standard; protein; 673 AA.

DE Human PRO polypeptide #8.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 248  
ID ADH97878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 249  
ID ADI01263 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 250  
ID ADI01958 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 251  
ID ADI03216 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 252  
ID ADI11403 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 253  
ID ADI02305 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 254  
ID ADI11743 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 255  
ID ADI05380 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 256  
ID ADH79452 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 257  
ID AD119409 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 258  
ID AD105210 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 259  
ID ADH79622 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 260  
ID AD101448 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 261  
ID AD101618 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 262  
ID AD101788 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 263  
ID ADH79792 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 264  
ID AD104610 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 265  
ID AD102746 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181651-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 266  
ID ADH78065 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 267  
ID AD125704 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 268  
ID AD125874 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 269  
ID ADK65386 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 270  
ID ADH98728 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191284-A1.  
PD 03-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 271  
ID ADH79969 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 272  
ID ADL93700 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 273  
ID ADC52154 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 274  
ID ADF35178 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.

Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 275  
ID ADG11428 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180853-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 276  
ID ADH06586 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 277  
ID ADH06416 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 278  
ID ADG68837 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 279  
ID ADH27727 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 280  
ID ADH25068 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 281  
ID ADH33700 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 282  
ID ADH02343 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 283  
ID ADH07950 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 284  
ID ADG69347 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 285  
ID ADH39168 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 286  
ID ADG83908 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 287  
ID ADH19298 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 288  
ID ADG85452 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 289  
ID ADH06246 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 290  
ID ADH30076 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 291  
ID ADH24388 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 292  
ID ADG69517 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 293  
ID ADH07780 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 294  
ID ADG85792 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 295  
ID ADH39338 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 296  
ID ADH33530 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 297  
ID ADH33870 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 298  
ID ADH01080 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 299  
ID ADG69687 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 300  
ID ADH20791 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 301  
ID ADH02173 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 302  
ID ADG69177 standard; protein; 673 AA.

DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 303  
ID ADG85962 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 304  
ID ADH24898 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 305  
ID ADH39515 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 306  
ID ADH19831 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 307  
ID ADH02513 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 308  
ID ADG69007 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 309  
ID ADH07610 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 310  
ID ADG86132 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 311  
ID ADH24728 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 312  
ID ADH25776 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 313  
ID ADH38342 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 314  
ID ADH57181 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 315  
ID ADH52169 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 316  
ID ADH49535 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 317  
ID ADH90497 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 318  
ID ADI11233 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 319  
ID ADH98898 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 320  
ID ADI02128 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003190699-A1.

PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 321  
ID ADH90667 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 322  
ID ADJ98542 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181797-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 323  
ID ADJ98712 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 324  
ID ADH78871 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 325  
ID ADJ99105 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 326  
ID ADJ99275 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 327  
ID ADJ98893 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 328  
ID ADH79041 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 329  
ID ADK00901 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003186407-A1.  
PD 02-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 330  
ID ADK14422 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 331  
ID ADM80871 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 332  
ID ADR45587 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 333  
ID ADY7711 standard; protein; 673 AA.  
DE Neoplastic disease detection protein PRO1282.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 98.4%; Score 3083.5; DB 9; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 334  
ID AE338367 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, #81.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 9; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 335  
ID AEF12542 standard; protein; 673 AA.  
DE Human PRO1282 protein SEQ ID NO:16.  
PN US2006008901-A1.  
PD 12-JAN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 10; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 336  
ID AEF74231 standard; protein; 673 AA.  
DE Human PRO1282 protein SEQ ID NO:16.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.

Query Match 98.4%; Score 3083.5; DB 10; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 337  
ID AEH43569 standard; protein; 673 AA.  
DE PRO1282 protein sequence, SEQ ID 16.  
PN US2006095657-A1.  
PD 11-MAY-2006.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 98.4%; Score 3083.5; DB 10; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 338  
ID AEJ11894 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2006160186-A1.  
PD 20-JUL-2006.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 98.4%; Score 3083.5; DB 10; Length 673;  
Best Local Similarity 88.7%; Pred. No. 9.1e-187;  
RESULT 339  
ID AAB84689 standard; protein; 673 AA.  
DE Amino acid sequence of human slit polypeptide Zslit3.  
PN WO200146418-A1.  
PD 28-JUN-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 98.2%; Score 3078.5; DB 4; Length 673;  
Best Local Similarity 88.6%; Pred. No. 1.9e-186;  
RESULT 340  
ID ADF69108 standard; protein; 673 AA.  
DE Human MP53 protein sequence SEQ ID NO:78.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 98.2%; Score 3078.5; DB 7; Length 673;  
Best Local Similarity 88.6%; Pred. No. 1.9e-186;  
RESULT 341  
ID AEL57287 standard; protein; 673 AA.  
DE Human glomerulus-specific marker, SEQ ID NO: 1750.  
PN US2006216722-A1.  
PD 28-SEP-2006.  
PA (BETS/) BETSHOLTZ C.  
PA (TRYG/) TRYGGVASON K.  
PA (TAKE/) TAKEMOTO M.  
PA (HELL/) HE L.  
PA (PATR/) PATRAKKAS J.  
Query Match 98.2%; Score 3078.5; DB 10; Length 673;  
Best Local Similarity 88.6%; Pred. No. 1.9e-186;  
RESULT 342  
ID ABO59449 standard; protein; 676 AA.  
DE Human genome derived single exon protein #5683.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 98.2%; Score 3078.5; DB 8; Length 676;  
Best Local Similarity 88.6%; Pred. No. 1.9e-186;  
RESULT 343

ID ADA57213 standard; protein; 672 AA.  
DE Human secreted protein #496.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.3e-177;  
RESULT 344  
ID ADA41092 standard; protein; 672 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.3e-177;  
RESULT 345  
ID ABR47923 standard; protein; 672 AA.  
DE Human secreted protein, SEQ ID 814.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.3e-177;  
RESULT 346  
ID AEL29423 standard; protein; 672 AA.  
DE Human secreted protein, SEQ ID 1403.  
PN US2006223088-A1.  
PD 05-OCT-2006.  
Query Match 93.8%; Score 2935; DB 10; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.3e-177;  
RESULT 347  
ID AEL94636 standard; protein; 672 AA.  
DE Human secreted protein amino acid sequence - SEQ ID 817.  
PN US2006246483-A1.  
PD 02-NOV-2006.  
Query Match 93.6%; Score 2935; DB 10; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.3e-177;  
RESULT 348  
ID AAB38323 standard; protein; 673 AA.  
DE Human secreted protein encoded by gene 3 clone HSYAV50.  
PN WO2000061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 3; Length 673;  
Best Local Similarity 85.2%; Pred. No. 2.3e-177;  
RESULT 349  
ID AAB38400 standard; peptide; 723 AA.  
DE Fragment of human secreted protein encoded by gene 3 clone HSYAV50.  
PN WO2000061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.8%; Score 2935; DB 3; Length 723;  
Best Local Similarity 85.2%; Pred. No. 2.5e-177;  
RESULT 350  
ID AAU75267 standard; protein; 630 AA.  
DE Human Slit-like protein #2.  
PN WO200212346-A2.  
PD 14-FEB-2002.  
PA (PHAA) PHARMACIA CORP.  
Query Match 90.8%; Score 2845.5; DB 5; Length 630;  
Best Local Similarity 85.2%; Pred. No. 1e-171;  
RESULT 351  
ID AAY66643 standard; protein; 611 AA.  
DE Membrane-bound protein PRO1282.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC.  
Query Match 86.5%; Score 2712.5; DB 3; Length 611;  
Best Local Similarity 79.5%; Pred. No. 2.6e-163;  
RESULT 352  
ID ABG78046 standard; protein; 673 AA.  
DE Mouse leucine-rich surface glycoprotein (LRSG-1).  
PN US2002072089-A1.

PD 13-JUN-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (MACB/) MACBETH K J.  
PA (BUSE/) BUSFIELD S J.  
PA (PAN/) PAN Y.  
PA (WHIT/) WHITE D.  
PA (KHOD/) KHODADOUST M M.  
PA (GUWW/) GU W.  
Query Match 79.4%; Score 2490; DB 5; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.6e-149;  
RESULT 353  
ID ADR45596 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 79.4%; Score 2490; DB 8; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.6e-149;  
RESULT 354  
ID AEL56067 standard; protein; 673 AA.  
DE Mouse slit-like 2, SEQ ID NO: 526.  
PN US2006216722-A1.  
PD 28-SEP-2006.  
PA (BETS/) BETSHOLTZ C.  
PA (TRYG/) TRYGGVASON K.  
PA (TAKE/) TAKEMOTO M.  
PA (HELL/) HE L.  
PA (PATR/) PATRAKAKS J.  
Query Match 79.4%; Score 2490; DB 10; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.6e-149;  
RESULT 355  
ID ADA00753 standard; protein; 673 AA.  
DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.  
PN WO2003018805-A1.  
PD 06-MAR-2003.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA (NINA-) JAPAN NAT CANCER CENT.  
Query Match 79.2%; Score 2484; DB 6; Length 673;  
Best Local Similarity 73.4%; Pred. No. 8.7e-149;  
RESULT 356  
ID AAB07431 standard; protein; 493 AA.  
DE A leucine-rich surface glycoprotein (LRSG).  
PN WO200042170-A1.  
PD 20-JUL-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 53.3%; Score 1672; DB 3; Length 493;  
Best Local Similarity 53.3%; Pred. No. 1.7e-97;  
RESULT 357  
ID ABB72324 standard; protein; 281 AA.  
DE Rat protein isolated from skin cells SEQ ID NO: 648.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 37.6%; Score 1178.5; DB 5; Length 281;  
Best Local Similarity 80.7%; Pred. No. 1.6e-66;  
RESULT 358  
ID AAO30403 standard; protein; 311 AA.  
DE Human secreted protein (SECP)-6.  
PN WO2003046196-A1.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.8%; Score 997.5; DB 7; Length 311;  
Best Local Similarity 68.7%; Pred. No. 5.3e-55;  
RESULT 359  
ID ABR58506 standard; protein; 307 AA.  
DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.  
PN WO2003029437-A2.  
PD 10-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.3%; Score 980.5; DB 6; Length 307;  
Best Local Similarity 67.9%; Pred. No. 6.2e-54;  
RESULT 360



ID AAO30821 standard; protein; 117 AA.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-11.  
FN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.0%; Score 471; DB 7; Length 117;  
Best Local Similarity 98.9%; Pred. No. 3.8e-22;  
RESULT 361  
ID AAE23980 standard; protein; 635 AA.  
DE Human LP220 secreted protein.  
FN WO200226801-A2.  
PD 04-APR-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 11.5%; Score 360.5; DB 5; Length 635;  
Best Local Similarity 27.1%; Pred. No. 2.7e-14;  
RESULT 362  
ID ABP70142 standard; protein; 647 AA.  
DE Human NOV44a.  
FN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.5%; Score 360.5; DB 5; Length 647;  
Best Local Similarity 27.1%; Pred. No. 2.8e-14;  
RESULT 363  
ID AAO26256 standard; protein; 635 AA.  
DE MDDT related human protein SEQ ID No 34.  
FN WO200296951-A1.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.5%; Score 359.5; DB 6; Length 635;  
Best Local Similarity 27.6%; Pred. No. 3.2e-14;  
RESULT 364  
ID AD209859 standard; protein; 635 AA.  
DE Human breast cancer marker MGC3103 protein.  
FN EPI522594-A2.  
PD 13-APR-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 11.5%; Score 359.5; DB 9; Length 635;  
Best Local Similarity 27.6%; Pred. No. 3.2e-14;  
RESULT 365  
ID ABP70144 standard; protein; 778 AA.  
DE Human NOV44c.  
FN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.4%; Score 357.5; DB 5; Length 778;  
Best Local Similarity 26.7%; Pred. No. 5.4e-14;  
RESULT 366  
ID ADM90979 standard; protein; 545 AA.  
DE Human pharmaceutically useful protein SeqID 372.  
FN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Query Match 11.2%; Score 350.5; DB 8; Length 545;  
Best Local Similarity 27.9%; Pred. No. 9.9e-14;  
RESULT 367  
ID ABP70143 standard; protein; 566 AA.  
DE Human NOV44b.  
FN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.8%; Score 339; DB 5; Length 566;  
Best Local Similarity 26.9%; Pred. No. 5.5e-13;  
RESULT 368  
ID AAE17484 standard; protein; 551 AA.  
DE Human leucine-rich repeat-8 (ZLR8) protein #2.  
FN WO200202604-A2.  
PD 10-JAN-2002.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 10.8%; Score 338; DB 5; Length 551;  
Best Local Similarity 27.4%; Pred. No. 6.2e-13;  
RESULT 369  
ID ADI21104 standard; protein; 618 AA.  
DE Novel human protein #79.  
FN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 337; DB 7; Length 618;  
Best Local Similarity 27.2%; Pred. No. 8.2e-13;  
RESULT 370  
ID ADA23287 standard; protein; 653 AA.  
DE Human SECX polypeptide, SEC5 #1.  
FN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 10.7%; Score 337; DB 6; Length 653;  
Best Local Similarity 23.6%; Pred. No. 8.7e-13;  
RESULT 371  
ID AAB23033 standard; protein; 694 AA.  
DE Human SLIT protein-like splice variant, SECX 3352358-1.  
FN WO200053742-A2.  
PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.7%; Score 337; DB 3; Length 694;  
Best Local Similarity 23.8%; Pred. No. 9.4e-13;  
RESULT 372  
ID AAB23034 standard; protein; 590 AA.  
DE Human SLIT protein-like splice variant, SECX 3352358-2.  
FN WO200053742-A2.  
PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.6%; Score 333; DB 3; Length 590;  
Best Local Similarity 25.8%; Pred. No. 1.4e-12;  
RESULT 373  
ID ADA23289 standard; protein; 590 AA.  
DE Human SECX polypeptide, SEC6.  
FN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 10.6%; Score 333; DB 6; Length 590;  
Best Local Similarity 25.8%; Pred. No. 1.4e-12;  
RESULT 374  
ID ABG04827 standard; protein; 526 AA.  
DE Novel human diagnostic protein #4818.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.6%; Score 332; DB 4; Length 526;  
Best Local Similarity 26.9%; Pred. No. 1.4e-12;  
RESULT 375  
ID AAY28806 standard; protein; 653 AA.  
DE cc359.4 secreted protein.  
FN WO950405-A1.  
PD 07-OCT-1999.  
PA (GEMY) GENETICS INST INC.  
Query Match 10.5%; Score 330; DB 2; Length 653;  
Best Local Similarity 24.2%; Pred. No. 2.4e-12;  
RESULT 376  
ID AAY66694 standard; protein; 653 AA.  
DE Membrane-bound protein PRO1111.  
FN WO9663088-A2.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 3; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 377  
ID AAB24073 standard; protein; 653 AA.  
DE Human PRO1111 protein sequence SEQ ID NO:46.  
FN WO200053755-A2.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 3; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 378  
 ID AAU12390 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide sequence.  
 PN WO200140466-A2.  
 PD 07-JUN-2001.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 4; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 379  
 ID AAE09438 standard; protein; 653 AA.  
 DE Human ebgPRO331a protein.  
 PN WO200160850-A1.  
 PD 23-AUG-2001.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 Query Match 10.5%; Score 330; DB 4; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 380  
 ID AAB65217 standard; protein; 653 AA.  
 DE Human PRO1111 (UNQ554) protein sequence SRQ ID NO:229.  
 PN WO200073454-A1.  
 PD 07-DEC-2000.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 4; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 381  
 ID ABUS8032 standard; protein; 653 AA.  
 DE Human PRO polypeptide #64.  
 PN US2003027183-A1.  
 PD 06-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 382  
 ID ABUS9110 standard; protein; 653 AA.  
 DE Novel human secreted or transmembrane protein PRO1111.  
 PN US2002132252-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 383  
 ID ABUS2622 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003032023-A1.  
 PD 13-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 384  
 ID ABO17834 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003032156-A1.  
 PD 13-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 385  
 ID ABUS2622 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002160384-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 386  
 ID ABUS2622 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002160384-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 387  
 ID ABUS2622 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002160384-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 388  
 ID ABUS2622 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002160384-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 389  
 ID ABUS2622 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002160384-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 390  
 ID AAO23105 standard; protein; 653 AA.  
 DE NAG14 'human modifier of p53 pathway' protein.  
 PN WO2003035833-A2.  
 PD 01-MAY-2003.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 391  
 ID ABUS9869 standard; protein; 653 AA.  
 DE Novel secreted and transmembrane protein PRO1111.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 392  
 ID ABUS9257 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2003027162-A1.  
 PD 06-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 393  
 ID ABO25954 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 394  
 ID ABO25059 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein (PRO) #219.  
 PN US2003036179-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 395  
 ID ABUS963 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 396  
 ID ABUS2341 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.

ID ABUS1088 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003004311-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 388  
 ID ABUS2508 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003003531-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 389  
 ID ABUS6788 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003036180-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 390  
 ID AAO23105 standard; protein; 653 AA.  
 DE NAG14 'human modifier of p53 pathway' protein.  
 PN WO2003035833-A2.  
 PD 01-MAY-2003.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 391  
 ID ABUS9869 standard; protein; 653 AA.  
 DE Novel secreted and transmembrane protein PRO1111.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 392  
 ID ABUS9257 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2003027162-A1.  
 PD 06-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 393  
 ID ABO25954 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 394  
 ID ABO25059 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein (PRO) #219.  
 PN US2003036179-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 395  
 ID ABUS963 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 396  
 ID ABUS2341 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.

PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 397  
ID ABU59406 standard; protein; 653 AA.  
DE Novel human secreted or transmembrane protein PRO1344.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 398  
ID ABU67064 standard; protein; 653 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 399  
ID ABU92172 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 400  
ID ABU10878 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 401  
ID ABU81630 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 402  
ID ABU88569 standard; protein; 653 AA.  
DE Human secreted and transmembrane polypeptide PRO1111.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 403  
ID ABO34083 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 404  
ID ADA45957 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 405  
ID ADA76388 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 406  
ID ADA19038 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 407  
ID ADA61661 standard; protein; 653 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 408  
ID ADB19446 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 409  
ID ADB27987 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 410  
ID ADA86466 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 411  
ID ADB16030 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 412  
ID ADA37740 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US200308297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 413  
ID ADA47816 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 414  
ID ADA21426 standard; protein; 653 AA.  
DE Human secreted/transmembrane polypeptide PRO1111.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 415  
ID ADA10213 standard; protein; 653 AA.

DE Human secreted/transmembrane protein, PRO1111.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 416  
ID ADA67611 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 417  
ID ADB30618 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 418  
ID ADA85914 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 419  
ID ADA17757 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 420  
ID ADA97126 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 421  
ID ADA79430 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 422  
ID ADA87569 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 423  
ID ADB16771 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 424  
ID ADA27865 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 425  
ID ADA91863 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 426  
ID ADB14926 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 427  
ID ADB18887 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 428  
ID ADA94102 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 429  
ID ADB19998 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 430  
ID ADB13310 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 431  
ID ABO43367 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 432  
ID ADA94445 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 433  
ID ADA74564 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

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RESULT 434
ID ADB24797 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077113-A1.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 435
ID ADA82321 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 436
ID ADA75284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 437
ID ADA85362 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 438
ID ADA84810 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 439
ID ADB30066 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 440
ID ADA80594 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 441
ID ADA75836 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 442
ID ADA38670 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 443
ID ADA7061 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082702-A1.
DE Human PRO polypeptide #219.
PN US2003073210-A1.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 444
ID ADB25357 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 445
ID ADA93533 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 446
ID ADB26883 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 447
ID ADB31170 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 448
ID ADA92791 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 449
ID ADA61098 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 450
ID ADB24245 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 451
ID ADA96574 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 452
ID ADA81146 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082702-A1.
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 453
ID ADA96022 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 454
ID ADB26331 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 455
ID ADB21816 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 456
ID ADA77595 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 457
ID ADB18335 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 458
ID ADA87018 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 459
ID ADA88121 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 460
ID ADA46509 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 461
ID ADB28539 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 462
ID ADB29091 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 463
ID ABO53169 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 464
ID ADA77043 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 465
ID ADA22352 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 466
ID ADA8673 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 467
ID ADA97678 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 468
ID ADB27435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003022339-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 469
ID ADB22368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 470
ID ABO22539 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 471
ID ADA06518 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO polypeptide #64.

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PN US2003049638-A1.  
 PD 13-MAR-2003.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 472  
 ID ADA319211 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003059782-A1.  
 PD 27-MAR-2003.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 473  
 ID ADA67059 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003068793-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 474  
 ID ADB22920 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003077711-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 475  
 ID ADB23693 standard; protein; 653 AA.  
 DE Human PRO polypeptide SEQ ID NO 438.  
 PN US2003077712-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 476  
 ID ADA92415 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082712-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 477  
 ID ADB15478 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003087352-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 478  
 ID ADB38730 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082766-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 479  
 ID ADB96237 standard; protein; 653 AA.  
 DE Human PRO polypeptide #64.  
 PN US2003054403-A1.  
 PD 20-MAR-2003.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 480  
 ID ADB38178 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087347-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 481  
 ID ADB66650 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082689-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 482  
 ID ADB89730 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082698-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 483  
 ID ADB90462 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082762-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 484  
 ID ADB39563 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082764-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 485  
 ID ADB47186 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082687-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 486  
 ID ADB86793 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082697-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 487  
 ID ADB77398 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082696-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 488  
 ID ADB34555 standard; protein; 653 AA.  
 DE Human PRO polypeptide SEQ ID NO 438.  
 PN US2003077717-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 489  
 ID ADB35659 standard; protein; 653 AA.  
 DE Human PRO polypeptide SEQ ID NO 438.  
 PN US2003077719-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
 RESULT 490  
 ID ADB38178 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087347-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;

RESULT 490  
ID ADB34003 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US200307716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 491  
ID ADB35107 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US200307718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 492  
ID ADB36211 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US200307720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 493  
ID ADB46606 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 494  
ID ADC57709 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 495  
ID ADC55073 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 496  
ID ADC11940 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 497  
ID ADC56362 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003064375-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 498  
ID ADC07417 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003086647-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 499  
ID ADC11407 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003069403-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 500  
ID ADC50479 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 501  
ID ADC72026 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 502  
ID ADC60005 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 503  
ID ADC53012 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 504  
ID ADC57366 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 505  
ID ADC60557 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 506  
ID ADC51032 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 507  
ID ADC65559 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 508  
ID ADC54657 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;



RESULT 509  
ID ADC53618 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 510  
ID ADC59141 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 511  
ID ADC56019 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 512  
ID ADC58589 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 513  
ID ADC14529 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 514  
ID ADD08061 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 515  
ID ADD03263 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 516  
ID ADC90255 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 517  
ID ADC81886 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 518  
ID ADC69674 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194770-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 519  
ID ADC48563 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 520  
ID ADD10092 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 521  
ID ADD07528 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2002193259-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 522  
ID ADD04667 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 523  
ID ADC82419 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 524  
ID ADC80623 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 525  
ID ADD11130 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 526  
ID ADC48011 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 527  
ID ADD08599 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;

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Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 528
ID ADC80071 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 529
ID ADD06848 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 530
ID ADD09540 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 531
ID ADC83095 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 532
ID ADD41253 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 533
ID ADD52392 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 534
ID ADD53132 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 535
ID ADD53684 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 536
ID ADD55202 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 537
ID ADD56160 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.
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DE Human PRO polypeptide #64.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 538
ID ADD51840 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 539
ID ADD02639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 540
ID ADD02073 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 541
ID ADD54255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 542
ID ADD54598 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 543
ID ADD92572 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 544
ID ADD91468 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 545
ID ADE04082 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 546
ID ADE26752 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.
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PD 08-MAY-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 547
ID ADE32379 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 548
ID ADE22311 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 549
ID ADD79535 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 550
ID ADE42071 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 551
ID ADE17888 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 552
ID ADP92020 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 553
ID ADE33483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 554
ID ADE34035 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 555
ID ADD80087 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 556
ID ADD93124 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 557
ID ADE19544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 558
ID ADE18992 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 559
ID ADE43188 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 560
ID ADD95977 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 561
ID ADE22863 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 562
ID ADD78981 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 563
ID ADE26219 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 564
ID ADE32931 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 565
ID ADD80087 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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RESULT 565  
ID ADE42623 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 566  
ID ADD80639 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 567  
ID ADD89667 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 568  
ID ADE40951 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 569  
ID ADE04750 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 570  
ID ADE92879 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 571  
ID ADF67156 standard; protein; 653 AA.  
DE Human PRO1111 amino acid sequence SEQ ID NO:229.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 572  
ID ADG21588 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 573  
ID ADG32329 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 574

ID ADF97564 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 575  
ID ADG80628 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 576  
ID ADG80076 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 577  
ID ADH55368 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 578  
ID ADH55920 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 579  
ID ADI35410 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 580  
ID ADI64139 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 581  
ID ADI65088 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 582  
ID ADI63587 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 583  
ID ADH82001 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.

PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 584  
ID ADH99902 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 585  
ID ADH81449 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 586  
ID ADM82618 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 587  
ID ADN16017 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 588  
ID ADN16646 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 589  
ID ADN15465 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 590  
ID ADN14913 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 591  
ID ADC81175 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 592  
ID ADD76623 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003100087-A1.  
PD 29-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 593  
ID ADD87987 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 594  
ID ADD86391 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 595  
ID ADE75839 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 596  
ID ADE23415 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 597  
ID ADE23967 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 598  
ID ADE24610 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 599  
ID ADD87435 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 600  
ID ADE89301 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199082-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 601  
ID ADE18440 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 602  
ID ADE88749 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 603  
ID ADE94769 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 604  
ID ADE91180 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 605  
ID ADE35355 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 606  
ID ADE95321 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 607  
ID ADE93431 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 608  
ID ADF35012 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 609  
ID ADE92327 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 610  
ID ADE90628 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 611  
ID ADE91775 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 612  
ID ADG11605 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 613  
ID ADG02354 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 614  
ID ADG22140 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 615  
ID ADG20210 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 616  
ID ADF98116 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 617  
ID ADG24333 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 618  
ID ADF98687 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 619  
ID ADG03518 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 620  
ID ADE92327 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

ID ADF99239 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 621  
ID ADG16824 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 622  
ID ADG05283 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 623  
ID ADG19550 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 624  
ID ADG13387 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 625  
ID ADG08444 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 626  
ID ADG15614 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 627  
ID ADF97012 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 628  
ID ADG06197 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 629  
ID ADG23781 standard; protein; 653 AA.

DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 630  
ID ADG04070 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 631  
ID ADG24971 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 632  
ID ADG07268 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 633  
ID ADG07820 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 634  
ID ADG55315 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 635  
ID ADG60979 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 636  
ID ADG62083 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 637  
ID ADG8284 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 638  
ID ADG57523 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.

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PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 639
ID ADG56971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 640
ID ADG55867 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 641
ID ADG58627 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 642
ID ADG70993 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 643
ID ADG58075 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 644
ID ADG53659 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 645
ID ADG71545 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 646
ID ADG81732 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 647
ID ADH19475 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003228656-A1.
PD 11-DEC-2003.

PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 648
ID ADH30694 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 649
ID ADH12061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 650
ID ADG52483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 651
ID ADG54211 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 652
ID ADG81180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 653
ID ADG56419 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 654
ID ADH12685 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 655
ID ADH20968 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 656
ID ADG61531 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;

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Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 657  
ID ADH20008 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 658  
ID ADH28618 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 659  
ID ADG54763 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 660  
ID ADG59803 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 661  
ID ADI81227 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 662  
ID ADG09970 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 663  
ID ADI15441 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 664  
ID ADG09318 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 665  
ID ADI14773 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 666  
ID ADI18368 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 667  
ID ADJ63649 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 668  
ID ADJ77544 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 669  
ID ADJ65666 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 670  
ID ADM27802 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 671  
ID ADM42526 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 672  
ID ADM28388 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 673  
ID ADI95870 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 674  
ID ADI96422 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 675

ID ADS32374 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2004203125-A1.  
PD 14-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 676  
ID ADT03358 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004214269-A1.  
PD 28-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 677  
ID ADZ03409 standard; protein; 653 AA.  
DE Human secreted/transmembrane PRO1111 protein.  
PN US2005074837-A1.  
PD 07-APR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 678  
ID AEA38492 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #132.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 679  
ID AEA23332 standard; protein; 653 AA.  
DE Tumor antigen of hematopoietic origin TAH015.  
PN WO2005049075-A2.  
PD 02-JUN-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 680  
ID AEB14155 standard; protein; 653 AA.  
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.  
PN US2005153396-A1.  
PD 14-JUL-2005.  
PA (BAKE/) BAKER K P.  
PA (BERE/) BERESINI M.  
PA (DEFO/) DEFORGE L.  
PA (DESN/) DESNOYERS L.  
PA (FILV/) FILVAROFF E.  
PA (GAOW/) GAO W.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.  
PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 681  
ID AED86353 standard; protein; 653 AA.  
DE Human PRO amino acid sequence, seq id 438.  
PN US2005245730-A1.  
PD 03-NOV-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 682  
ID AEF79019 standard; protein; 653 AA.

DE Human NAG14 polypeptide SEQ ID NO: 2.  
PN US2006035826-A1.  
PD 16-FEB-2006.  
PA (LINJ/) LIN J C.  
PA (ROSE/) ROSENTHAL A.  
Query Match 10.5%; Score 330; DB 10; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 683  
ID AEG58300 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide SEQ ID NO: 438.  
PN US2006073568-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 10; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 684  
ID AEI43945 standard; protein; 653 AA.  
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 438.  
PN US2006040351-A1.  
PD 23-FEB-2006.  
PA (BAKE/) BAKER K P.  
PA (BERE/) BERESINI M.  
PA (DEFO/) DEFORGE L.  
PA (DESN/) DESNOYERS L.  
PA (FILV/) FILVAROFF E.  
PA (GAOW/) GAO W.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.  
PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Query Match 10.5%; Score 330; DB 10; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 685  
ID AEI24028 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111, SEQ ID NO:438.  
PN EP1672070-A2.  
PD 21-JUN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 10; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.4e-12;  
RESULT 686  
ID ABU12069 standard; protein; 775 AA.  
DE Human NOV15a CG92531-01 protein SEQ ID 58.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.5%; Score 329.5; DB 6; Length 775;  
Best Local Similarity 26.0%; Pred. No. 3.2e-12;  
RESULT 687  
ID AEG98014 standard; protein; 649 AA.  
DE Human leucine rich repeat domain protein associated protein #1.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.5%; Score 329; DB 5; Length 649;  
Best Local Similarity 24.6%; Pred. No. 2.8e-12;  
RESULT 688  
ID ADS98753 standard; protein; 824 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 10.5%; Score 329; DB 8; Length 824;  
Best Local Similarity 25.5%; Pred. No. 3.7e-12;  
RESULT 689

ID ABG34079 standard; protein; 627 AA.  
DE Human Pro peptide #51.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 5; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 690  
ID ADA01368 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 691  
ID ADA43797 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 692  
ID ADA43565 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003073196-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 693  
ID ADA01240 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 694  
ID ADA01124 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 695  
ID ADA43681 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 696  
ID ADA06943 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 697  
ID ADA08431 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 698  
ID ADB99724 standard; protein; 627 AA.

DE Human PRO polypeptide SEQ ID 100.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 699  
ID ADB7007 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003082726-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 700  
ID ADB66162 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 701  
ID ADB99840 standard; protein; 627 AA.  
DE Human PRO polypeptide SEQ ID 100.  
PN US2003073192-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 702  
ID ADB99495 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 703  
ID ADB66046 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 704  
ID ADC23444 standard; protein; 627 AA.  
DE Human transmembrane PRO polypeptide (SeqID 100).  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 705  
ID ADC26137 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 706  
ID ADE04964 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 707  
ID ADE11270 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.

PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 708  
ID ADD88201 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 709  
ID ADD95496 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 710  
ID ADE06426 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 711  
ID ADE38201 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 712  
ID ADD88317 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 713  
ID ADD90898 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 714  
ID ADF99453 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 715  
ID ADG06546 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 716  
ID ADG05497 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077741-A1.

PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 717  
ID ADG82498 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 718  
ID ADE51751 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 719  
ID ADE51867 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 720  
ID ADE37725 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 721  
ID ADE37609 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 722  
ID ADD95380 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 723  
ID ADE38080 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 724  
ID ADE76169 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 725  
ID ADE39492 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119117-A1.  
PD 26-JUN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 726  
ID ADE04296 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide #50.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 727  
ID ADE39893 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 728  
ID ADE19758 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 729  
ID ADE77336 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 730  
ID ADE65444 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 731  
ID ADE76053 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 732  
ID ADE37964 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 733  
ID ADE64574 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 734  
ID ADE38909 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 735  
ID ADE51983 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 736  
ID ADD91014 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 737  
ID ADE38793 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 738  
ID ADE37493 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 739  
ID ADE06309 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 740  
ID ADD90169 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 741  
ID ADE38677 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 742  
ID ADE39608 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 743  
ID ADD89213 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;

Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 744  
ID ADH8980 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 745  
ID ADE19874 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 746  
ID ADE77452 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 747  
ID ADE65328 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 748  
ID ADE39376 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 749  
ID ADE38561 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 750  
ID ADG1114 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 751  
ID ADG10998 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 752  
ID ADH31526 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 753  
ID ADH38774 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 754  
ID ADH29409 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 755  
ID ADH23712 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 756  
ID ADH27042 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 757  
ID ADH38310 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 758  
ID ADH26926 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 759  
ID ADH38194 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 760  
ID ADH38890 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 761  
ID ADH23828 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 762  
ID ADH31526 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;

ID ADH40203 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 763  
ID ADH40088 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 764  
ID ADH31410 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 765  
ID ADH29288 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 766  
ID ADH49503 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 767  
ID ADH51967 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 768  
ID ADH49822 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 769  
ID ADH52423 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 770  
ID ADH52539 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 771  
ID ADH58536 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 772  
ID ADH51851 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 773  
ID ADH58412 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 774  
ID ADL13609 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 775  
ID ADK00865 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US20031186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 776  
ID ADL08606 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US20031186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 777  
ID AEG75266 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2006073579-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 10; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 778  
ID AEG74481 standard; protein; 627 AA.  
DE Human PRO34192 protein SEQ ID NO:100.  
PN US2006073553-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 10; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 779  
ID AEG73353 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2006073551-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 10; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
RESULT 780  
ID AEG74597 standard; protein; 627 AA.  
DE Human PRO34192 polypeptide SEQ ID NO:100.

PN US2006073552-A1.  
 PD 06-APR-2006.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 328.5; DB 10; Length 627;  
 Best Local Similarity 24.2%; Pred. No. 2.9e-12;  
 RESULT 781  
 ID AAU32870 standard; protein; 636 AA.  
 DE Novel human secreted protein #3361.  
 PN WO200179449-A2.  
 PD 25-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 10.4%; Score 327.5; DB 4; Length 636;  
 Best Local Similarity 24.4%; Pred. No. 3.4e-12;  
 RESULT 782  
 ID ABO84499 standard; protein; 626 AA.  
 DE Mouse cancer-associated protein MP14-035.1.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 10.3%; Score 324; DB 8; Length 626;  
 Best Local Similarity 24.3%; Pred. No. 5.5e-12;  
 RESULT 783  
 ID AAG65805 standard; protein; 628 AA.  
 DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.  
 PN WO200172827-A2.  
 PD 04-OCT-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 10.3%; Score 324; DB 4; Length 628;  
 Best Local Similarity 24.1%; Pred. No. 5.6e-12;  
 RESULT 784  
 ID ADN95165 standard; protein; 810 AA.  
 DE Human BEC/LBC-related protein sequence SeqID87.  
 PN WO2003080640-A1.  
 PD 02-OCT-2003.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN ) LICENTIA LTD.  
 Query Match 10.3%; Score 322.5; DB 7; Length 810;  
 Best Local Similarity 22.0%; Pred. No. 9.3e-12;  
 RESULT 785  
 ID ABR59642 standard; protein; 811 AA.  
 DE Human cancer related protein SEQ ID NO:299.  
 PN WO2003025138-A2.  
 PD 27-MAR-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 10.3%; Score 322.5; DB 6; Length 811;  
 Best Local Similarity 22.0%; Pred. No. 9.3e-12;  
 RESULT 786  
 ID AAO23114 standard; protein; 811 AA.  
 DE KIAA0644 'human modifier of p53 pathway' protein.  
 PN WO2003035833-A2.  
 PD 01-MAY-2003.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.3%; Score 322.5; DB 6; Length 811;  
 Best Local Similarity 22.0%; Pred. No. 9.3e-12;  
 RESULT 787  
 ID ADN95110 standard; protein; 811 AA.  
 DE Human LEC protein sequence SeqID32.  
 PN WO2003080640-A1.  
 PD 02-OCT-2003.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN ) LICENTIA LTD.  
 Query Match 10.3%; Score 322.5; DB 7; Length 811;  
 Best Local Similarity 22.0%; Pred. No. 9.3e-12;  
 RESULT 788  
 ID ADQ21196 standard; protein; 811 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 10.3%; Score 322.5; DB 8; Length 811;  
 Best Local Similarity 22.0%; Pred. No. 9.3e-12;  
 RESULT 789  
 ID ABL77006 standard; protein; 811 AA.

DE Toll-like receptor/Interleukin-1 receptor 14 (TLR14) SEQ ID NO 1.  
 PN WO2006111946-A2.  
 PD 26-OCT-2006.  
 PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
 Query Match 10.3%; Score 322.5; DB 10; Length 811;  
 Best Local Similarity 22.0%; Pred. No. 9.3e-12;  
 RESULT 790  
 ID ADR45590 standard; protein; 605 AA.  
 DE Homologue of LRSG-1, baboon ALS.  
 PN US2004176296-A1.  
 PD 09-SEP-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 10.3%; Score 322; DB 8; Length 605;  
 Best Local Similarity 36.2%; Pred. No. 7.1e-12;  
 RESULT 791  
 ID AAG67523 standard; protein; 628 AA.  
 DE Amino acid sequence of a human secreted polypeptide.  
 PN WO200166690-A2.  
 PD 13-SEP-2001.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 Query Match 10.2%; Score 321; DB 4; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 792  
 ID AAB84469 standard; protein; 628 AA.  
 DE Amino acid sequence of an interferon omega-1 like protein NOV2.  
 PN WO200142471-A2.  
 PD 14-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 10.2%; Score 321; DB 4; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 793  
 ID ABP69326 standard; protein; 628 AA.  
 DE Human polypeptide SEQ ID NO 1373.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 10.2%; Score 321; DB 5; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 794  
 ID ADF69107 standard; protein; 628 AA.  
 DE Human MP53 protein sequence SEQ ID NO:77.  
 PN WO2003083047-A2.  
 PD 09-OCT-2003.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.2%; Score 321; DB 7; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 795  
 ID ADH71652 standard; protein; 628 AA.  
 DE Human protein of the invention NOV22a SEQ ID NO:548.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 10.2%; Score 321; DB 8; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 796  
 ID ADH71654 standard; protein; 628 AA.  
 DE Human protein of the invention NOV22b SEQ ID NO:550.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 10.2%; Score 321; DB 8; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 797  
 ID ABO84502 standard; protein; 628 AA.  
 DE Human cancer-associated protein HP14-035.3.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 10.2%; Score 321; DB 8; Length 628;  
 Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
 RESULT 798  
 ID ABO84503 standard; protein; 628 AA.



DE Human cancer-associated protein HP14-035.4.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
RESULT 799  
ID ABO84501 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8.6e-12;  
RESULT 800  
ID ABP70928 standard; protein; 762 AA.  
DE Human LP341 protein.  
PN WO2003029778-A2.  
PD 10-APR-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 10.2%; Score 321; DB 6; Length 762;  
Best Local Similarity 25.5%; Pred. No. 1.1e-11;  
RESULT 801  
ID ADI36917 standard; protein; 797 AA.  
DE Human LRR protein #12.  
PN US2003220263-A1.  
PD 27-NOV-2003.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 10.2%; Score 321; DB 8; Length 797;  
Best Local Similarity 25.5%; Pred. No. 1.1e-11;  
RESULT 802  
ID ADS98018 standard; protein; 803 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 10.2%; Score 321; DB 8; Length 803;  
Best Local Similarity 25.5%; Pred. No. 1.1e-11;  
RESULT 803  
ID AAY13349 standard; protein; 660 AA.  
DE Amino acid sequence of protein PRO265.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 2; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 804  
ID ADC78348 standard; protein; 660 AA.  
DE Human PRO265 protein.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 3; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 805  
ID AAB80217 standard; protein; 660 AA.  
DE Human PRO265 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 806  
ID AAB31208 standard; protein; 660 AA.  
DE Amino acid sequence of human polypeptide PRO265.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 807  
ID AAU12346 standard; protein; 660 AA.  
DE Human PRO265 polypeptide sequence.  
PN WO2001040466-A2.  
PD 07-JUN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 808  
ID ABB84839 standard; protein; 660 AA.  
DE Human PRO265 protein sequence SEQ ID NO:46.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 5; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 809  
ID ABB95445 standard; protein; 660 AA.  
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.2%; Score 320; DB 5; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 810  
ID ABU71595 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 811  
ID ABO17790 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 812  
ID ABU71450 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 813  
ID ABO25179 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 814  
ID ABU81044 standard; protein; 660 AA.

DE Human PRO polypeptide #175.  
 PN US2003004311-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 815  
 ID ABU71896 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein PRO265.  
 PN US2003003530-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 816  
 ID ABO01779 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 817  
 ID ABU66744 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003036180-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 818  
 ID ABU54352 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein PRO265.  
 PN US2002132240-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 819  
 ID ABU67297 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003032063-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 820  
 ID AAO23116 standard; protein; 660 AA.  
 DE FLRT2 'human modifier of p53 pathway' protein.  
 PN WO2003035833-A2.  
 PD 01-MAY-2003.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 821  
 ID ABO47367 standard; protein; 660 AA.  
 DE Human secreted/transmembrane polypeptide PRO265.  
 PN US2003044839-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 822  
 ID ABUS9825 standard; protein; 660 AA.  
 DE Novel secreted and transmembrane protein PRO265.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 823  
 ID ABO25015 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein (PRO) #175.  
 PN US2003004311-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 824  
 ID ABU64504 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2002160374-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 825  
 ID ABU72065 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2002177165-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 826  
 ID ABU67350 standard; protein; 660 AA.  
 DE Human secreted protein PRO265.  
 PN US2003023054-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 827  
 ID ABU67166 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003032062-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 828  
 ID ABO14870 standard; protein; 660 AA.  
 DE Human secreted / transmembrane polypeptide PRO265.  
 PN US2003036060-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 829  
 ID ABU67020 standard; protein; 660 AA.  
 DE Human secreted/transmembrane, PRO, protein SEQ ID 350.  
 PN US2003032155-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 830  
 ID ABU69627 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003017463-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 831  
 ID ABU79808 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein PRO265.  
 PN US2003032057-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 832  
 ID ABO14809 standard; protein; 660 AA.  
 DE Human secreted / transmembrane polypeptide PRO265.  
 PN US2003027143-A1.

PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 833  
 ID ADA45869 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003022328-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 834  
 ID ADA76300 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003073212-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 835  
 ID ADB29233 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003092002-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 836  
 ID ADA18950 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003054517-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 837  
 ID ADA61573 standard; protein; 660 AA.  
 DE Homo sapiens.  
 PN US2003049816-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 838  
 ID ADB19358 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003068796-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 839  
 ID ADB27899 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003082704-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 840  
 ID ADA86378 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082711-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 841  
 ID ADB15942 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003087350-A1.  
 PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 842  
 ID ADA47728 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003073215-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 843  
 ID ADA18089 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003039971-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 844  
 ID ABO32761 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein PRO265.  
 PN US2003045693-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 845  
 ID ADA67523 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003068795-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 846  
 ID ADB30530 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003068794-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 847  
 ID ADA85826 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082693-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 848  
 ID ADA97038 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003082705-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 849  
 ID ADA79342 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003082763-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 850  
 ID ADA87481 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003087345-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 851  
 ID ADBi6683 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003087349-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 852  
 ID ABO34821 standard; protein; 660 AA.  
 DE Human PRO polypeptide #6.  
 PN US2003044793-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 853  
 ID ADA16064 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003049621-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 854  
 ID ADA91775 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082694-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 855  
 ID ADBi4838 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003087351-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 856  
 ID ADA47287 standard; protein; 660 AA.  
 DE Human secreted/transmembrane polypeptide PRO265.  
 PN US2003044844-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 857  
 ID ADBi8799 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003073211-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 858  
 ID ADA94014 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003077722-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 859  
 ID ADBi9910 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082691-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;

Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 860  
 ID ADBi3222 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003082710-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 861  
 ID ABO43323 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003044945-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 862  
 ID ADA74476 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003068798-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 863  
 ID ADA42209 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003054401-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 864  
 ID ADB24709 standard; protein; 660 AA.  
 DE Human PRO polypeptide SEQ ID NO 350.  
 PN US2003077713-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 865  
 ID ADA82233 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003082701-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 866  
 ID ADA75196 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003073216-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 867  
 ID ADA85274 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082695-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 868  
 ID ADA84722 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082708-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
 RESULT 869  
 ID ADBi9910 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003082691-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 6; Length 660;

RESULT 869  
ID ABO17499 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 870  
ID ADB29978 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 871  
ID ADA80506 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 872  
ID ADA75748 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 873  
ID ADA46973 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 874  
ID ADB25269 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US200307715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 875  
ID ADA93445 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 876  
ID ADB26795 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 877  
ID ADB31082 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 878  
ID ADA86930 standard; protein; 660 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 879  
ID ADB24157 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US200307714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 880  
ID ADA96486 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 881  
ID ADA81058 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 882  
ID ADA95934 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 883  
ID ADB26243 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 884  
ID ADB21728 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 885  
ID ADA77507 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 886  
ID ADB18247 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US200307710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 887  
ID ADA86930 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 888  
ID ADA16488 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 889  
ID ADA12917 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 890  
ID ADA41785 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 891  
ID ADA98033 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 892  
ID ADA46421 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 893  
ID ADA17132 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 894  
ID ADA42635 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 895  
ID ADB28451 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 896  
ID ADB29003 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.

PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 897  
ID ADA76955 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 898  
ID ADA88585 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 899  
ID ADA97590 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 900  
ID ADB27347 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 901  
ID ADB22280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 902  
ID ABO19866 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 903  
ID ABO17560 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 904  
ID ADA66971 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 905  
ID ADB22832 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 906
ID ADB23605 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 907
ID ADA92327 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 908
ID ADB15390 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 909
ID ADB38642 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 910
ID ADB38090 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 911
ID ADB66562 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 912
ID ADB89642 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 913
ID ADB30374 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 914
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 915
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 916
ID ADB74690 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 917
ID ADB47098 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 918
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 919
ID ADB77310 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 920
ID ADB34467 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 921
ID ADB35571 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 922
ID ADB33915 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 923
ID ADB35019 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 924
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 7; Length 660;
RESULT 925
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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RESULT 924  
ID ADB36123 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US200307720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 925  
ID ADB46518 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US200308262-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 926  
ID ADC28336 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 927  
ID ADC39536 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 928  
ID ADC40050 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 929  
ID ADC18878 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 930  
ID ADC34174 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 931  
ID ADC29229 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 932  
ID ADC28760 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 933

ID ADC40645 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 934  
ID ADC19302 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 935  
ID ADC33750 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 936  
ID ADC12820 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 937  
ID ADC50391 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 938  
ID ADC71938 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 939  
ID ADC59917 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 940  
ID ADC52924 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 941  
ID ADC57278 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 942  
ID ADC60469 standard; protein; 660 AA.



DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 943  
ID ADC50944 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 944  
ID ADC65471 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 945  
ID ADC54569 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 946  
ID ADC35330 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 947  
ID ADC59053 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 948  
ID ADC55931 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 949  
ID ADC8501 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 950  
ID ADC12272 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 951  
ID ADD03175 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 952  
ID ADC90167 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 953  
ID ADC69586 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 954  
ID ADC48475 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 955  
ID ADD10004 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 956  
ID ADD04579 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 957  
ID ADC80535 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 958  
ID ADD11042 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 959  
ID ADD10335 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 960  
ID ADC47923 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194771-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 961  
ID ADD04827 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 962  
ID ADC79983 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 963  
ID ADD11295 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 964  
ID ADD09452 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 965  
ID ADD03833 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 966  
ID ADD03409 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 967  
ID ADD04165 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 968  
ID ADD52304 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 969  
ID ADD53044 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194792-A1.  
PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 970  
ID ADD53596 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 971  
ID ADD37088 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 972  
ID ADD51752 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 973  
ID ADD02551 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 974  
ID ADD01985 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 975  
ID ADD54167 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 976  
ID ADD92484 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 977  
ID ADD91380 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 978  
ID ADE03994 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 979  
ID ADE32291 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 980  
ID ADE22223 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 981  
ID ADD79447 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 982  
ID ADE41983 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 983  
ID ADE17800 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 984  
ID ADD91932 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 985  
ID ADE33395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 986  
ID ADE33947 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 987  
ID ADD79999 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;

Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 988  
ID ADD93036 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 989  
ID ADE19456 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 990  
ID ADE34661 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 991  
ID ADE18904 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 992  
ID ADE43100 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 993  
ID ADD95889 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 994  
ID ADE22775 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 995  
ID ADD78893 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 996  
ID ADE32843 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;

RESULT 997  
ID ADG42535 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 998  
ID ADD80551 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 999  
ID ADH89579 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1000  
ID ADH40863 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1001  
ID ADS04662 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1002  
ID ADE92791 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1003  
ID ADG21500 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1004  
ID ADG23141 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1005  
ID ADF97476 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1006

ID ADG80540 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1007  
ID ADG79988 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1008  
ID ADG63796 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1009  
ID ADH59144 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1010  
ID ADH55280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1011  
ID ADH55832 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1012  
ID ADI37923 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1013  
ID ADI65000 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1014  
ID ADI63499 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1015  
ID ADH81913 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1016  
ID ADH81361 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1017  
ID ADJ26191 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1018  
ID ADH82530 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1019  
ID ADN15929 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1020  
ID ADN16558 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1021  
ID ADN15377 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1022  
ID ADN14825 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1023  
ID ADI64051 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1024  
ID ADC81087 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092108-A1.

PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1025  
ID ADE79106 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1026  
ID ADD76535 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1027  
ID ADD87899 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1028  
ID ADD86303 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1029  
ID ADE79530 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1030  
ID ADE75751 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1031  
ID ADE73206 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1032  
ID ADE41296 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1033  
ID ADE23327 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003092108-A1.

PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1034  
ID ADE23879 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1035  
ID ADE24522 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1036  
ID ADB87347 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1037  
ID ADE89213 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1038  
ID ADE41210 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003104558-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1039  
ID ADE73741 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1040  
ID ADE18352 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1041  
ID ADE88661 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1042  
ID ADE99295 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003211576-A1.  
PD 13-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1043  
ID ADE94681 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1044  
ID ADE91092 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1045  
ID ADE95233 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1046  
ID ADE93343 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1047  
ID ADF34924 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1048  
ID ADE98414 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1049  
ID ADE92239 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1050  
ID ADE90540 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1051  
ID ADE91687 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1052
ID ADE98841 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1053
ID ADG40311 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US200325253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1054
ID ADF73705 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1055
ID ADG02266 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1056
ID ADG22052 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1057
ID ADG20122 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1058
ID ADF98028 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1059
ID ADG24245 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1060
ID ADG15526 standard; protein; 660 AA.

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ID ADF98599 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1061
ID ADG03430 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1062
ID ADF99151 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1063
ID ADG16736 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1064
ID ADG05195 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1065
ID ADG19462 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1066
ID ADF73281 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1067
ID ADG13299 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1068
ID ADG08356 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1069
ID ADG15526 standard; protein; 660 AA.

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DE Human PRO polypeptide #175.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1070
ID ADF96324 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1071
ID ADG06109 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1072
ID ADG23693 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1073
ID ADG03982 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1074
ID ADG24983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1075
ID ADG07180 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1076
ID ADG07732 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1077
ID ADG55227 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1078
ID ADG60891 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207146-A1.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1079
ID ADG61995 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1080
ID ADG92124 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1081
ID ADG82196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1082
ID ADG57435 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1083
ID ADG56883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1084
ID ADG55779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1085
ID ADG58539 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1086
ID ADG70905 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1087
ID ADG92551 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003207146-A1.
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PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1088  
ID ADG57987 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1089  
ID ADG53571 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1090  
ID ADG71457 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1091  
ID ADG81644 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1092  
ID ADH30606 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US200307723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1093  
ID ADG63645 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1094  
ID ADH11973 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1095  
ID ADG52395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1096  
ID ADG54123 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1097  
ID ADG81092 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1098  
ID ADG56331 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1099  
ID ADH12597 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1100  
ID ADG61443 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1101  
ID ADH28530 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1102  
ID ADG54675 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1103  
ID ADG59715 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1104  
ID ADH20340 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1105  
ID ADH43479 standard; protein; 660 AA.  
DE Human PRO polypeptide #23.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;



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Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1122
ID ADM24995 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1123
ID ADJ63561 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1124
ID ADM29741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1125
ID ADJ77456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1126
ID ADX82824 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1127
ID ADJ65578 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1128
ID ADM27714 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1129
ID ADM42438 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1130
ID ADO06063 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1131
ID ADM28300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1132
ID ADR10915 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1133
ID ADR17824 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANG/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1134
ID ADI95782 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1135
ID ADI96334 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1136
ID ADI65657 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1137
ID ADS74463 standard; protein; 660 AA.

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DE Human secreted/transmembrane protein #7.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1138
ID ADS32286 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1139
ID ADT03270 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1140
ID ADT03500 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1141
ID ADU06386 standard; protein; 660 AA.
DE Novel bronchial cancer-associated human protein SeqID610.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1142
ID ADZ03321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1143
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1144
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1145
ID AED23772 standard; protein; 660 AA.
DE Human secreted protein PRO 265, SEQ ID 28.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1146
ID AED86265 standard; protein; 660 AA.
DE Human PRO amino acid sequence, seq id 350.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1147
ID AEE68941 standard; protein; 660 AA.
DE Fibromodulin homologous PRO265 protein, SEQ ID 28.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 10; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1148
ID AEG58212 standard; protein; 660 AA.
DE Human PRO265 polypeptide SEQ ID NO: 350.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 10; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1149
ID AEI43857 standard; protein; 660 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 350.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.

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PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.  
PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Query Match 10.2%; Score 320; DB 10; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1150  
ID AEI23940 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265, SEQ ID NO:350.  
PN EP1672070-A2.  
PD 21-JUN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 10; Length 660;  
Best Local Similarity 22.4%; Pred. No. 1.1e-11;  
RESULT 1151  
ID ADT77808 standard; protein; 452 AA.  
DE Chimeric Nogo receptor polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 10.2%; Score 318.5; DB 8; Length 452;  
Best Local Similarity 27.3%; Pred. No. 8.4e-12;  
RESULT 1152  
ID ADT77802 standard; protein; 452 AA.  
DE Chimeric Nogo receptor polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 10.1%; Score 317.5; DB 10; Length 648;  
Best Local Similarity 25.0%; Pred. No. 1.5e-11;  
RESULT 1154  
ID AAEI3006 standard; protein; 713 AA.  
DE Human leucine-rich repeat (LRR) family member protein.  
PN WO200175105-A2.  
PD 11-OCT-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 317.5; DB 4; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.7e-11;  
RESULT 1155  
ID AAU91335 standard; protein; 713 AA.  
DE Human novel secreted protein LP223(a).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.1%; Score 316.5; DB 5; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.9e-11;  
RESULT 1156  
ID ABG97991 standard; protein; 713 AA.  
DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.1%; Score 316.5; DB 5; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.9e-11;  
RESULT 1157  
ID ABUS2381 standard; protein; 713 AA.  
DE Human GPCR related protein NOV31a.

PN WO200279398-A2.  
PD 10-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.1%; Score 316.5; DB 6; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.9e-11;  
RESULT 1158  
ID AEI93171 standard; protein; 713 AA.  
DE Novel human secreted protein, LP223(a).  
PN US2006147945-A1.  
PD 06-JUL-2006.  
PA (EDMO/) EDMONDS B T.  
PA (MICA/) MICANOVIC R.  
PA (OUWW/) OU W.  
PA (SUEW/) SU E W.  
PA (TSCB/) TSCHANG S R.  
PA (WANG/) WANG H.  
Query Match 10.1%; Score 316.5; DB 10; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.9e-11;  
RESULT 1159  
ID ADT77796 standard; protein; 474 AA.  
DE Chimeric Nogo receptor polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 10.0%; Score 314.5; DB 8; Length 474;  
Best Local Similarity 27.8%; Pred. No. 1.6e-11;  
RESULT 1160  
ID AAU91341 standard; protein; 656 AA.  
DE Human novel secreted protein LP223(b).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.0%; Score 313.5; DB 5; Length 656;  
Best Local Similarity 23.6%; Pred. No. 2.7e-11;  
RESULT 1161  
ID AEI93183 standard; protein; 656 AA.  
DE Novel human secreted protein, LP223(b).  
PN US2006147945-A1.  
PD 06-JUL-2006.  
PA (EDMO/) EDMONDS B T.  
PA (MICA/) MICANOVIC R.  
PA (OUWW/) OU W.  
PA (SUEW/) SU E W.  
PA (TSCB/) TSCHANG S R.  
PA (WANG/) WANG H.  
Query Match 10.0%; Score 313.5; DB 10; Length 656;  
Best Local Similarity 23.8%; Pred. No. 2.7e-11;  
RESULT 1162  
ID ADL24097 standard; protein; 713 AA.  
DE Human NOVX polypeptide #71.  
PN US2004002120-A1.  
PD 01-JAN-2004.  
PA (KEKU/) KEKUDA R.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (MALV/) MALYANKAR U M.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (CASM/) CASMAN S J.  
PA (PENA/) PENA C E A.  
PA (GANG/) GANGOLLI E A.  
PA (GUSE/) GUSEV V Y.  
PA (SMIT/) SMITHSON G.

PA (ZERH/) ZERHUSEN B D.  
PA (GERL/) GERLACH V.  
PA (POCH/) POCHART P F.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (RAST/) RASTELLI L.  
PA (SPAD/) SPADERNA S K.  
PA (LARO/) LAROCHELLE W J.  
PA (ZHON/) ZHONG M.  
PA (KHRA/) KHRAMTSOV N V.  
PA (VOSS/) VOSS E Z.  
PA (HERR/) HERMANN J L.  
Query Match  
Best Local Similarity 10.0%; Score 313.5; DB 8; Length 713;  
Best Local Similarity 23.1%; Pred. No. 3e-11;  
RESULT 1163  
ID AAE09437 standard; protein; 592 AA.  
DE Human sbgTango79a protein.  
PN WO200160850-A1.  
PD 23-AUG-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 4; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1164  
ID AAE25351 standard; protein; 592 AA.  
DE Human LP polypeptide, LP243.  
PN WO200248361-A2.  
PD 20-JUN-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1165  
ID AAU91329 standard; protein; 592 AA.  
DE Human novel secreted protein LP243(b).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1166  
ID ABP60996 standard; protein; 592 AA.  
DE Novel human protein. SEQ ID 83.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1167  
ID AAU79167 standard; protein; 592 AA.  
DE Human leucine-rich repeat proteins-like protein NOVA.  
PN WO200214368-A2.  
PD 21-FEB-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1168  
ID ABG74693 standard; protein; 592 AA.  
DE Human CGDD protein 6803363CD1 SEQ ID 19.  
PN WO2003014322-A2.  
PD 20-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 6; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1169  
ID ADE03417 standard; protein; 592 AA.  
DE Human immunoglobulin superfamily member BGS-2.  
PN US2003195163-A1.  
PD 16-OCT-2003.  
PA (WUSS/) WU S.  
PA (KRYST) KRYSTEK S R.  
PA (LEEL/) LEE L.

PA (FEDE/) FEDER J N.  
PA (CHEN/) CHENG J D.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 7; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1170  
ID ADU02709 standard; protein; 592 AA.  
DE Novel human polypeptide seqid 1176.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 8; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1171  
ID AEI93159 standard; protein; 592 AA.  
DE Novel human secreted protein, LP243(b).  
PN US2006147945-A1.  
PD 06-JUL-2006.  
PA (EDMO/) EDMONDS B T.  
PA (MICA/) MICANOVIC R.  
PA (OUWM/) OU W.  
PA (SUEW/) SU E W.  
PA (TSCH/) TSCHANG S R.  
PA (WANG/) WANG H.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 10; Length 592;  
Best Local Similarity 25.9%; Pred. No. 3e-11;  
RESULT 1172  
ID ABG61770 standard; protein; 608 AA.  
DE Novel leucine-rich protein.  
PN WO200229058-A2.  
PD 11-APR-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 608;  
Best Local Similarity 25.9%; Pred. No. 3.1e-11;  
RESULT 1173  
ID ABG97967 standard; protein; 634 AA.  
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 9.9%; Score 311; DB 5; Length 634;  
Best Local Similarity 24.1%; Pred. No. 3.7e-11;  
RESULT 1174  
ID ABR55628 standard; protein; 420 AA.  
DE Amino acid sequence of rat Nogo-66 receptor homologue NGRH1.  
PN WO2003035687-A1.  
PD 01-MAY-2003.  
PA (NOVS) NOVARTIS AG.  
PA (NOVS) NOVARTIS PHARMA GMBH.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 420;  
Best Local Similarity 29.8%; Pred. No. 2.5e-11;  
RESULT 1175  
ID ADT77788 standard; protein; 420 AA.  
DE Rat Nogo receptor 2 polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UVRP) UNIV ROCHESTER.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 420;  
Best Local Similarity 29.8%; Pred. No. 2.5e-11;  
RESULT 1176  
ID AAO23115 standard; protein; 674 AA.  
DE FLRT1 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 674;  
Best Local Similarity 21.5%; Pred. No. 4.3e-11;  
RESULT 1177  
ID ADH17606 standard; protein; 674 AA.  
DE Human NOV19a protein - SEQ ID 296.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;

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Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1178
ID ADH17628 standard; protein; 674 AA.
DE Human NOV191 protein - SEQ ID 318.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1179
ID ADH17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1180
ID ADH17634 standard; protein; 674 AA.
DE Human NOV19o protein - SEQ ID 324.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1181
ID ADH17632 standard; protein; 674 AA.
DE Human NOV19n protein - SEQ ID 322.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1182
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1183
ID ABO34232 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1184
ID AAU29215 standard; protein; 649 AA.
DE Human PRO polypeptide sequence #192.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1185
ID AAB70533 standard; protein; 649 AA.
DE Human PRO3 protein sequence SEQ ID NO:6.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1186
ID AAB87591 standard; protein; 649 AA.
DE Human PRO1865.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1187
ID ABE95916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1188
ID ABB84953 standard; protein; 649 AA.
DE Human PRO1865 protein sequence SEQ ID NO:274.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1189
ID ABP70109 standard; protein; 649 AA.
DE Human NOV27a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1190
ID ABB95559 standard; protein; 649 AA.
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1191
ID ABU58591 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1192
ID ABU88139 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1193
ID ABU84454 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1194
ID ABR66328 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027278-A1.
PD 06-FEB-2003.
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Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1195  
ID ABR65718 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1196  
ID ABU99658 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1197  
ID ABU82897 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1198  
ID ABU90018 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1199  
ID ABR68267 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1200  
ID ABU96320 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1201  
ID ABU92751 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1202  
ID ABO08828 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1203  
ID ABO02880 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1204  
ID ABR75034 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1205

ID ABR94796 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1206  
ID ABU85769 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1207  
ID ABU98929 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1208  
ID ABU98144 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1209  
ID ABU91850 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1210  
ID ABU9543 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1211  
ID ABU86384 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1212  
ID ABU67597 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1213  
ID ABU80625 standard; protein; 649 AA.  
DE Human PRO protein #192.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1214  
ID ABU90941 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;



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Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1215
ID ABO34000 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1216
ID ABR99543 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1217
ID ABR98933 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1218
ID ABO16456 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1219
ID ABR92356 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1220
ID ABO18997 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1221
ID ABR78418 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1222
ID ABU72017 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1223
ID ABU85154 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1224
ID ABO00293 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1225
ID ABO11625 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1226
ID ABO02270 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1227
ID ABU8844 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1228
ID ASU83539 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1229
ID ABO06340 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1230
ID ABR59376 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1231
ID ABO09438 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1232
ID ABO19302 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1233
ID ABO11320 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1234
ID ABR66938 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1235
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ID ABO16151 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1236  
ID ABO13857 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1237  
ID ABU71571 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1238  
ID ABU65760 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein, SEQ ID 384.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1239  
ID ABO07608 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1240  
ID ABO03795 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1241  
ID ABR67243 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1242  
ID ABO15846 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1243  
ID ABUS6127 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein, PRO1865.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1244  
ID ABU72352 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1245

ID ABU5455 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1246  
ID ABU95400 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1247  
ID ABU71303 standard; protein; 649 AA.  
DE Human PRO1865 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1248  
ID ABO07913 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1249  
ID ABR70154 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1250  
ID ABR69487 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1251  
ID ABO01628 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1252  
ID ABU81430 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1253  
ID ABR60227 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1254  
ID ABU91025 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1255

ID ABR67962 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1256  
ID ABR65350 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1257  
ID ABR68572 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1258  
ID ABR71984 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1259  
ID ABU85464 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1260  
ID ABU89154 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1261  
ID ABU83234 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1262  
ID ABU95090 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1263  
ID ABU90638 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1264  
ID ABU84149 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1265  
ID ABU93800 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003040066-A1.  
PD 27-FEB-2003.

PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1266  
ID ABR65045 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1267  
ID ABR68877 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1268  
ID ABO06693 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1269  
ID ABR99238 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1270  
ID ASU57122 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1271  
ID ABU86074 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1272  
ID ABU82361 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1273  
ID ABU87372 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1274  
ID ABU83844 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 5.2e-11;  
RESULT 1275  
ID ABO08218 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003040066-A1.  
PD 27-FEB-2003.

Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1276  
ID ABU92541 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein PRO1865.  
PN US2003045684-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1277  
ID ABU91929 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1278  
ID ABU66093 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1279  
ID ABU81211 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1280  
ID ABR59922 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1281  
ID ABU94110 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1282  
ID ABU99963 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1283  
ID ABR66633 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1284  
ID ABR91051 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1285  
ID ABO53325 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003027986-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1286  
ID ABU94478 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1287  
ID ABU79360 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1288  
ID ABU86689 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1289  
ID ABU86994 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1290  
ID ABU94783 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1291  
ID ABO04710 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1292  
ID ABR70459 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1293  
ID ABU98624 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1294  
ID ABR66023 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1295  
ID ABR64740 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1296  
ID ABU79665 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1297  
ID ABU93056 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1298  
ID ABU96015 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1299  
ID ABU91235 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1300  
ID ABU90328 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1301  
ID ABO09743 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1302  
ID ABO11015 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1303  
ID ABR71069 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1304  
ID ABU98328 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1305  
ID ABU87677 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1306

ID ABU91545 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US20030321128-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1307  
ID ABU9333 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1308  
ID ABU84759 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1309  
ID ABR69849 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1310  
ID ABU80226 standard; protein; 649 AA.  
DE Human PRO protein #192.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1311  
ID ABU82540 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1312  
ID ABU93495 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1313  
ID ABO10048 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1314  
ID ABO09133 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1315  
ID ABU96504 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1316

ID ABU10701 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein #192.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1317  
ID ABU72174 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1318  
ID ABU95710 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1319  
ID ABU96919 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1320  
ID ABR70764 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1321  
ID ABO05115 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1322  
ID ABO08523 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1323  
ID ABO05730 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1324  
ID ABR74119 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1325  
ID ABR95711 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1326  
ID ABR81008 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1327  
ID ABR81313 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1328  
ID ABO01009 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1329  
ID ABR88611 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003088743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1330  
ID ABO05115 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1331  
ID ABO28916 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1332  
ID ABO08523 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1333  
ID ABO31661 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1334  
ID ABO40558 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1335  
ID ABR95711 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;

RESULT 1335  
ID ABO35983 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1336  
ID ABO44122 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1337  
ID ADA78136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1338  
ID ABM24917 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1339  
ID ABO03185 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1340  
ID ABR30441 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1341  
ID ABM17355 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1342  
ID ABR95101 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1343  
ID ABR95406 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1344  
ID ADB17189 standard; protein; 649 AA.  
DE Human transmembrane PRO polypeptide (SeqID 132).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1345  
ID ABO21644 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1346  
ID ABR97908 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1347  
ID ABR87696 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1348  
ID ABM77737 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1349  
ID ABM27967 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1350  
ID ABM06248 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003088704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1351  
ID ABM03754 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1352  
ID ABM35205 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1353  
ID ABM26442 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;

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Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1354
ID ABO48224 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1355
ID ABR92966 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1356
ID ABO24727 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1357
ID ABM11738 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1358
ID ABM02839 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1359
ID ABM16135 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1360
ID ABO27696 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1361
ID ABM29187 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1362
ID ABM07163 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1363
ID ABM21257 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1364
ID ABM09603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1365
ID ABO41473 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1366
ID ABO36288 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1367
ID ABO43817 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1368
ID ABM76517 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1369
ID ABM76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1370
ID ABM25832 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1371
ID ABM26137 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1372
ID ABO03490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036127-A1.
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PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1373  
ID ABO02575 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1374  
ID ABO44304 standard; protein; 649 AA.  
DE Human secreted/transmembrane polypeptide PRO 1865.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1375  
ID ABR90746 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1376  
ID ABR73814 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1377  
ID ABO17066 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1378  
ID ABR94491 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1379  
ID ABR75998 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1380  
ID ABR71374 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1381  
ID ABR93271 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1382  
ID ABR93576 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1383  
ID ABR88001 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1384  
ID ABO28001 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1385  
ID ABO30136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1386  
ID ABO33345 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1387  
ID ABO5033 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1388  
ID ABO08993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1389  
ID ABO36593 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1390  
ID ABO35678 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1391  
ID ABO39643 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1392  
ID ABM10518 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1393  
ID ABM12043 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1394  
ID ABO52189 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1395  
ID ABO52494 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1396  
ID ADA19994 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1397  
ID ABO23812 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1398  
ID ADB17377 standard; protein; 649 AA.  
DE Human transmembrane PRO polypeptide (SeqID 132).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1399  
ID ABR97298 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1400  
ID ABR87086 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1401  
ID ABM11128 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1402  
ID ABM28272 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1403  
ID ABO32271 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003088733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1404  
ID ABM15398 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1405  
ID ABO6553 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1406  
ID ABO4364 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003088716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1407  
ID ABO22477 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1408  
ID ABO7773 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1409  
ID ABO40863 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1410
ID ABM35510 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1411
ID ABM32723 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1412
ID AB052799 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1413
ID AB050359 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1414
ID AB099353 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1415
ID AB004405 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1416
ID AB006035 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1417
ID ABM18575 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1418
ID ABR97603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1419
ID ABR80703 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1420
ID ABR01314 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1421
ID ABR88916 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1422
ID ABR13568 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1423
ID ABM20952 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1424
ID ABO42083 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1425
ID ABO42693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1426
ID ABM10213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1427
ID ABO38728 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003086773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1428
ID ABM32968 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073185-A1.
PD 17-APR-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1429  
ID ABM22782 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1430  
ID ABM74993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1431  
ID ADA79928 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1432  
ID ABR96383 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1433  
ID ABM02534 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1434  
ID ABR86476 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1435  
ID ABR86781 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1436  
ID ABM16745 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1437  
ID ABM29797 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1438  
ID ABO29221 standard; protein; 649 AA.

DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1439  
ID ABM24002 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1440  
ID ABM23392 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1441  
ID ABM22172 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1442  
ID ABO37813 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1443  
ID ABM28577 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1444  
ID ABM28882 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1445  
ID ABM66526 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1446  
ID ABM75908 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1447  
ID ABM34188 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003096359-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1448  
ID ABR34493 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1449  
ID ABO20424 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1450  
ID ABO21339 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1451  
ID ABO22254 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1452  
ID ABR96688 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1453  
ID ABR96688 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1454  
ID ABR85866 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1455  
ID ABR99848 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1456  
ID ABR00399 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1457

ID ABR00704 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1458  
ID ABO29831 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1459  
ID ABR23697 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1460  
ID ABR29492 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1461  
ID ABO38423 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1462  
ID ABO45723 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1463  
ID ABR20647 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1464  
ID ADA81655 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1465  
ID ABO16761 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1466  
ID ABO18387 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044920-A1.

PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1467  
ID ABO22814 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1468  
ID ABO23119 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1469  
ID ABR92661 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1470  
ID ABR81618 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1471  
ID ABM78042 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1472  
ID ABR89831 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1473  
ID ABM26747 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1474  
ID ABM13873 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1475  
ID ABO28611 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1476

ID ABO30441 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1477  
ID ABM07468 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1478  
ID ABM04059 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1479  
ID ABO37203 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1480  
ID ABO41778 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1481  
ID ABO35373 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1482  
ID ABM25222 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1483  
ID ABO47614 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1484  
ID ABO47919 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 5.2e-11;  
RESULT 1485  
ID ABO48529 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1486  
ID ABO51579 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1487  
ID ABO51884 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1488  
ID ABO50664 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1489  
ID ABR79788 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1490  
ID ABM17050 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1491  
ID ABO18082 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US200304918-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1492  
ID ABO21034 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1493  
ID ABR96993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1494  
ID ABM12348 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1495  
ID ABM16440 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1496  
ID ABM24307 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1497  
ID ABM14788 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1498  
ID ABM04669 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1499  
ID ABM06858 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;  
RESULT 1500  
ID ABM09298 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;

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 OM protein - protein search, using sw model  
 Run on: August 29, 2007, 08:46:46 ; Search time 75 Seconds  
 (without alignments)  
 1138.492 Million cell updates/sec

Title: US-09-943-780-69  
 Perfect score: 3135  
 Sequence: 1 MCSRVPLLLPLLLALLGPG.....PLMGFPGLQSPHAKPYI 598

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 983262 seqs, 14278483 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

Database : Issued Patents AA:  
 1: /EMC Celerra\_SID52/ptodata/1/iaa/5 COMB.pep.\*  
 2: /EMC Celerra\_SID52/ptodata/1/iaa/6 COMB.pep.\*  
 3: /EMC Celerra\_SID52/ptodata/1/iaa/7 COMB.pep.\*  
 4: /EMC Celerra\_SID52/ptodata/1/iaa/H COMB.pep.\*  
 5: /EMC Celerra\_SID52/ptodata/1/iaa/RTUS COMB.pep.\*  
 6: /EMC Celerra\_SID52/ptodata/1/iaa/RE COMB.pep.\*  
 7: /EMC Celerra\_SID52/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3135	100.0	598	2	US-09-866-028-69 Sequence 69, Appl
2	3135	100.0	598	2	US-09-944-457-69 Sequence 69, Appl
3	3135	100.0	598	2	US-09-945-584-69 Sequence 69, Appl
4	3135	100.0	598	2	US-09-944-944-69 Sequence 69, Appl
5	3135	100.0	598	2	US-09-945-587-69 Sequence 69, Appl
6	3135	100.0	598	3	US-09-944-884-69 Sequence 69, Appl
7	3135	100.0	598	3	US-10-219-074-104 Sequence 104, App
8	3135	100.0	598	3	US-10-227-873-104 Sequence 104, App
9	3135	100.0	598	3	US-10-218-849-104 Sequence 104, App
10	3135	100.0	598	3	US-10-216-168-104 Sequence 104, App
11	3135	100.0	598	3	US-09-944-896-69 Sequence 69, Appl
12	3083.5	98.4	673	2	US-09-063-950-2 Sequence 2, Appl1
13	3083.5	98.4	673	2	US-09-991-181-52 Sequence 52, Appl
14	3083.5	98.4	673	2	US-09-990-444-52 Sequence 52, Appl
15	3083.5	98.4	673	2	US-09-997-333-52 Sequence 52, Appl
16	3083.5	98.4	673	2	US-09-992-598-52 Sequence 52, Appl
17	3083.5	98.4	673	2	US-09-989-735-52 Sequence 52, Appl
18	3083.5	98.4	673	3	US-09-989-726-52 Sequence 52, Appl
19	3083.5	98.4	673	3	US-09-997-514-52 Sequence 52, Appl
20	3083.5	98.4	673	3	US-09-989-728-52 Sequence 52, Appl
21	3083.5	98.4	673	3	US-09-997-349-52 Sequence 52, Appl
22	3083.5	98.4	673	3	US-09-997-653-52 Sequence 52, Appl
23	3083.5	98.4	673	3	US-09-989-293A-52 Sequence 52, Appl
24	3083.5	98.4	673	3	US-09-989-732-52 Sequence 52, Appl
25	3083.5	98.4	673	3	US-09-990-441-52 Sequence 52, Appl
26	3083.5	98.4	673	3	US-09-989-328-52 Sequence 52, Appl

27	3083.5	98.4	673	3	US-09-989-724-52 Sequence 52, Appl
28	3083.5	98.4	673	3	US-09-989-733-52 Sequence 52, Appl
29	3083.5	98.4	673	3	US-09-993-583-52 Sequence 52, Appl
30	3083.5	98.4	673	3	US-10-063-639A-16 Sequence 16, Appl
31	3083.5	98.4	673	3	US-09-989-279-52 Sequence 52, Appl
32	3083.5	98.4	673	3	US-09-991-157-52 Sequence 52, Appl
33	3083.5	98.4	673	3	US-10-063-638A-16 Sequence 16, Appl
34	3083.5	98.4	673	3	US-10-063-510-16 Sequence 16, Appl
35	3083.5	98.4	673	3	US-09-990-439-52 Sequence 52, Appl
36	3083.5	98.4	673	3	US-09-997-641-52 Sequence 52, Appl
37	3083.5	98.4	673	3	US-10-063-741-16 Sequence 16, Appl
38	3083.5	98.4	673	3	US-10-063-584-16 Sequence 16, Appl
39	3083.5	98.4	673	3	US-09-997-384-52 Sequence 52, Appl
40	3083.5	98.4	673	3	US-09-989-730-52 Sequence 52, Appl
41	3083.5	98.4	673	3	US-10-066-867-16 Sequence 16, Appl
42	3083.5	98.4	673	3	US-09-997-585-52 Sequence 52, Appl
43	3083.5	98.4	673	3	US-10-063-659-16 Sequence 16, Appl
44	3083.5	98.4	673	3	US-10-063-742-16 Sequence 16, Appl
45	3083.5	98.4	673	3	US-10-063-703-16 Sequence 16, Appl
46	3083.5	98.4	673	3	US-10-063-709-16 Sequence 16, Appl
47	3083.5	98.4	673	3	US-10-063-581-16 Sequence 16, Appl
48	3083.5	98.4	673	3	US-10-063-583-16 Sequence 16, Appl
49	3083.5	98.4	673	3	US-10-063-593-16 Sequence 16, Appl
50	3083.5	98.4	673	3	US-09-997-601-52 Sequence 52, Appl
51	3083.5	98.4	673	3	US-10-063-599-16 Sequence 16, Appl
52	3083.5	98.4	673	3	US-10-063-660-16 Sequence 16, Appl
53	3083.5	98.4	673	3	US-10-063-647-16 Sequence 16, Appl
54	3083.5	98.4	673	3	US-10-063-647-16 Sequence 16, Appl
55	3083.5	98.4	673	3	US-10-063-661-16 Sequence 16, Appl
56	3083.5	98.4	673	3	US-10-063-651-16 Sequence 16, Appl
57	3083.5	98.4	673	3	US-10-063-530-16 Sequence 16, Appl
58	3083.5	98.4	673	3	US-10-063-540-16 Sequence 16, Appl
59	3083.5	98.4	673	3	US-10-063-648-16 Sequence 16, Appl
60	3083.5	98.4	673	3	US-10-063-657-16 Sequence 16, Appl
61	3083.5	98.4	673	3	US-10-063-702-16 Sequence 16, Appl
62	3083.5	98.4	673	3	US-10-063-529-16 Sequence 16, Appl
63	3083.5	98.4	673	3	US-10-063-644-16 Sequence 16, Appl
64	3083.5	98.4	673	3	US-10-063-585-16 Sequence 16, Appl
65	3083.5	98.4	673	3	US-10-063-591A-16 Sequence 16, Appl
66	3083.5	98.4	673	3	US-10-063-516-16 Sequence 16, Appl
67	3083.5	98.4	673	3	US-10-063-532-16 Sequence 16, Appl
68	3083.5	98.4	673	3	US-10-063-654-16 Sequence 16, Appl
69	3083.5	98.4	673	3	US-10-063-582-16 Sequence 16, Appl
70	3083.5	98.4	673	3	US-10-063-524-16 Sequence 16, Appl
71	3083.5	98.4	673	3	US-10-972-317-16 Sequence 16, Appl
72	3083.5	98.4	673	3	US-10-063-551-16 Sequence 16, Appl
73	3083.5	98.4	673	3	US-10-063-650-16 Sequence 16, Appl
74	3083.5	98.4	673	3	US-10-063-523-16 Sequence 16, Appl
75	3083.5	98.4	673	3	US-10-063-592A-16 Sequence 16, Appl
76	3083.5	98.4	673	3	US-10-063-705-16 Sequence 16, Appl
77	3083.5	98.4	673	3	US-10-063-598-16 Sequence 16, Appl
78	3083.5	98.4	673	3	US-10-063-554-16 Sequence 16, Appl
79	3083.5	98.4	673	3	US-10-063-597-16 Sequence 16, Appl
80	3083.5	98.4	673	3	US-10-063-600-16 Sequence 16, Appl
81	3083.5	98.4	673	3	US-10-063-652A-16 Sequence 16, Appl
82	3083.5	98.4	673	3	US-10-063-602-16 Sequence 16, Appl
83	3083.5	98.4	673	3	US-10-063-560-16 Sequence 16, Appl
84	3083.5	98.4	673	3	US-10-063-517-16 Sequence 16, Appl
85	3083.5	98.4	673	3	US-10-063-548-16 Sequence 16, Appl
86	3083.5	98.4	673	3	US-10-063-553-16 Sequence 16, Appl
87	3083.5	98.4	673	3	US-10-063-653A-16 Sequence 16, Appl
88	3083.5	98.4	673	3	US-10-063-595-16 Sequence 16, Appl
89	3083.5	98.4	673	3	US-10-063-587-16 Sequence 16, Appl
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93	337	10.7	653	2	US-09-957-187-10 Sequence 10, Appl
94	337	10.7	653	2	US-09-991-053-10 Sequence 10, Appl
95	333	10.6	590	2	US-09-520-781-12 Sequence 12, Appl
96	333	10.6	590	2	US-09-957-187-12 Sequence 12, Appl
97	333	10.6	590	2	US-09-991-053-12 Sequence 12, Appl
98	330	10.5	653	2	US-09-991-181-229 Sequence 229, App
99	330	10.5	653	2	US-09-990-444-229 Sequence 229, App



100	330	10.5	653	2	US-09-997-333-229	Sequence 229, App	173	320	10.2	660	3	US-09-906-838B-28	Sequence 28, Appl
101	330	10.5	653	2	US-09-992-598-229	Sequence 229, App	174	320	10.2	660	3	US-09-909-320-28	Sequence 28, Appl
102	330	10.5	653	2	US-09-989-735-229	Sequence 229, App	175	320	10.2	660	3	US-10-152-398-350	Sequence 350, App
103	330	10.5	653	3	US-09-989-726-229	Sequence 229, App	176	320	10.2	660	3	US-10-123-907-350	Sequence 350, App
104	330	10.5	653	3	US-09-997-514-229	Sequence 229, App	177	320	10.2	660	3	US-10-147-512-350	Sequence 350, App
105	330	10.5	653	3	US-09-989-728-229	Sequence 229, App	178	320	10.2	660	3	US-09-907-942-28	Sequence 28, Appl
106	330	10.5	653	3	US-09-997-349-229	Sequence 229, App	179	320	10.2	660	3	US-09-906-815C-28	Sequence 28, Appl
107	330	10.5	653	3	US-09-997-653-229	Sequence 229, App	180	320	10.2	660	3	US-10-147-485-350	Sequence 350, App
108	330	10.5	653	3	US-09-989-293A-229	Sequence 229, App	181	320	10.2	660	3	US-10-124-814-350	Sequence 350, App
109	330	10.5	653	3	US-09-989-732-229	Sequence 229, App	182	320	10.2	660	3	US-10-124-822-350	Sequence 350, App
110	330	10.5	653	3	US-09-990-441-229	Sequence 229, App	183	320	10.2	660	3	US-10-223-081-46	Sequence 46, Appl
111	330	10.5	653	3	US-10-123-292-438	Sequence 438, App	184	320	10.2	660	3	US-10-223-087-46	Sequence 46, Appl
112	330	10.5	653	3	US-09-989-328-229	Sequence 229, App	185	320	10.2	660	3	US-10-131-833A-350	Sequence 350, App
113	330	10.5	653	3	US-09-989-724-229	Sequence 229, App	186	320	10.2	660	3	US-09-903-749A-28	Sequence 28, Appl
114	330	10.5	653	3	US-09-989-733-229	Sequence 229, App	187	320	10.2	660	3	US-09-904-532B-28	Sequence 28, Appl
115	330	10.5	653	3	US-09-993-583-229	Sequence 229, App	188	320	10.2	660	3	US-10-142-419-350	Sequence 350, App
116	330	10.5	653	3	US-10-152-398-438	Sequence 438, App	189	320	10.2	660	3	US-10-152-375-350	Sequence 350, App
117	330	10.5	653	3	US-09-989-279-229	Sequence 229, App	190	320	10.2	660	3	US-10-223-082-46	Sequence 46, Appl
118	330	10.5	653	3	US-10-123-907-438	Sequence 438, App	191	320	10.2	660	3	US-10-223-084-46	Sequence 46, Appl
119	330	10.5	653	3	US-10-147-512-438	Sequence 438, App	192	320	10.2	660	3	US-10-131-818A-350	Sequence 350, App
120	330	10.5	653	3	US-10-147-485-438	Sequence 438, App	193	320	10.2	660	3	US-09-905-075-28	Sequence 28, Appl
121	330	10.5	653	3	US-09-991-157-229	Sequence 229, App	194	320	10.2	660	3	US-10-145-873-350	Sequence 350, App
122	330	10.5	653	3	US-10-124-814-438	Sequence 438, App	195	320	10.2	660	3	US-10-152-395-350	Sequence 350, App
123	330	10.5	653	3	US-10-124-822-438	Sequence 438, App	196	320	10.2	660	3	US-10-131-822A-350	Sequence 350, App
124	330	10.5	653	3	US-09-990-439-229	Sequence 229, App	197	320	10.2	660	3	US-10-142-763-350	Sequence 350, App
125	330	10.5	653	3	US-09-997-641-229	Sequence 229, App	198	320	10.2	660	3	US-10-128-694A-350	Sequence 350, App
126	330	10.5	653	3	US-09-997-384-229	Sequence 229, App	199	320	10.2	660	3	US-10-123-213-350	Sequence 350, App
127	330	10.5	653	3	US-10-131-833A-438	Sequence 438, App	200	320	10.2	660	3	US-10-123-909-350	Sequence 350, App
128	330	10.5	653	3	US-10-142-419-438	Sequence 438, App	201	320	10.2	660	3	US-10-131-826A-350	Sequence 350, App
129	330	10.5	653	3	US-09-989-730-229	Sequence 229, App	202	320	10.2	660	3	US-09-903-640A-28	Sequence 28, Appl
130	330	10.5	653	3	US-10-152-375-438	Sequence 438, App	203	320	10.2	660	3	US-10-448-580-28	Sequence 28, Appl
131	330	10.5	653	3	US-09-997-585-229	Sequence 229, App	204	320	10.2	660	3	US-10-147-513-350	Sequence 350, App
132	330	10.5	653	3	US-10-131-818A-438	Sequence 438, App	205	320	10.2	660	3	US-10-121-043-350	Sequence 350, App
133	330	10.5	653	3	US-10-145-873-438	Sequence 438, App	206	320	10.2	660	3	US-10-963-467-28	Sequence 28, Appl
134	330	10.5	653	3	US-10-152-395-438	Sequence 438, App	207	320	10.2	660	3	US-10-448-923-28	Sequence 28, Appl
135	330	10.5	653	3	US-10-131-822A-438	Sequence 438, App	208	320	10.2	660	3	US-10-139-980-350	Sequence 350, App
136	330	10.5	653	3	US-10-142-763-438	Sequence 438, App	209	320	10.2	660	3	US-10-223-090-46	Sequence 46, Appl
137	330	10.5	653	3	US-10-128-694A-438	Sequence 438, App	210	320	10.2	683	2	US-09-949-016-7267	Sequence 7267, Ap
138	330	10.5	653	3	US-09-997-601-229	Sequence 229, App	211	312	10.0	592	3	US-10-193-477-2	Sequence 2, Appl1
139	330	10.5	653	3	US-10-123-213-438	Sequence 438, App	212	310.5	9.9	674	2	US-09-689-486-59	Sequence 59, Appl
140	330	10.5	653	3	US-10-123-909-438	Sequence 438, App	213	310.5	9.9	674	2	US-09-689-486-60	Sequence 60, Appl
141	330	10.5	653	3	US-10-131-826A-438	Sequence 438, App	214	310.5	9.9	674	2	US-09-973-424A-59	Sequence 59, Appl
142	330	10.5	653	3	US-10-147-513-438	Sequence 438, App	215	310.5	9.9	674	2	US-09-973-424A-60	Sequence 60, Appl
143	330	10.5	653	3	US-10-121-043-438	Sequence 438, App	216	310.5	9.9	674	2	US-09-973-424A-75	Sequence 75, Appl
144	330	10.5	653	3	US-09-997-666-229	Sequence 229, App	217	310	9.9	662	2	US-09-949-016-10298	Sequence 10298, A
145	330	10.5	653	3	US-10-139-980-438	Sequence 438, App	218	309	9.9	649	3	US-10-063-638A-132	Sequence 132, App
146	328.5	10.5	627	3	US-10-245-913-100	Sequence 100, App	219	309	9.9	649	3	US-10-183-001-384	Sequence 384, App
147	328.5	10.5	627	3	US-10-245-752-100	Sequence 100, App	220	309	9.9	649	3	US-10-180-998-384	Sequence 384, App
148	328.5	10.5	627	3	US-10-242-095-100	Sequence 100, App	221	309	9.9	649	3	US-10-201-769-384	Sequence 132, App
149	328.5	10.5	627	3	US-10-242-652-100	Sequence 100, App	222	309	9.9	649	3	US-10-063-638A-132	Sequence 132, App
150	322	10.3	605	2	US-09-063-950-5	Sequence 5, Appl1	223	309	9.9	649	3	US-10-063-510-132	Sequence 274, App
151	321	10.2	797	3	US-10-424-233-16	Sequence 16, Appl	224	309	9.9	649	3	US-10-223-081-274	Sequence 274, App
152	320	10.2	660	2	US-09-907-794A-28	Sequence 28, Appl	225	309	9.9	649	3	US-10-063-741-132	Sequence 132, App
153	320	10.2	660	2	US-09-905-125A-28	Sequence 28, Appl	226	309	9.9	649	3	US-10-063-584-132	Sequence 132, App
154	320	10.2	660	2	US-09-902-775A-28	Sequence 28, Appl	227	309	9.9	649	3	US-10-174-576-384	Sequence 384, App
155	320	10.2	660	2	US-09-906-700-28	Sequence 28, Appl	228	309	9.9	649	3	US-10-223-087-274	Sequence 274, App
156	320	10.2	660	2	US-09-903-603A-28	Sequence 28, Appl	229	309	9.9	649	3	US-10-174-581-384	Sequence 384, App
157	320	10.2	660	2	US-09-904-520A-28	Sequence 28, Appl	230	309	9.9	649	3	US-10-006-867-132	Sequence 132, App
158	320	10.2	660	2	US-09-949-016-6843	Sequence 6843, Ap	231	309	9.9	649	3	US-10-223-082-274	Sequence 274, App
159	320	10.2	660	2	US-09-909-064-28	Sequence 28, Appl	232	309	9.9	649	3	US-10-223-084-274	Sequence 274, App
160	320	10.2	660	2	US-09-905-381A-28	Sequence 28, Appl	233	309	9.9	649	3	US-10-063-659-132	Sequence 132, App
161	320	10.2	660	2	US-09-906-618-28	Sequence 28, Appl	234	309	9.9	649	3	US-10-063-742-132	Sequence 132, App
162	320	10.2	660	2	US-09-906-646-28	Sequence 28, Appl	235	309	9.9	649	3	US-10-063-703-132	Sequence 132, App
163	320	10.2	660	2	US-09-689-486-58	Sequence 58, Appl	236	309	9.9	649	3	US-10-063-709-132	Sequence 132, App
164	320	10.2	660	2	US-09-904-462-28	Sequence 28, Appl	237	309	9.9	649	3	US-10-063-581-132	Sequence 132, App
165	320	10.2	660	2	US-09-904-654-28	Sequence 28, Appl	238	309	9.9	649	3	US-10-063-583-132	Sequence 132, App
166	320	10.2	660	2	US-09-906-722A-28	Sequence 28, Appl	239	309	9.9	649	3	US-10-063-593-132	Sequence 132, App
167	320	10.2	660	2	US-09-905-449-28	Sequence 28, Appl	240	309	9.9	649	3	US-10-063-599-132	Sequence 132, App
168	320	10.2	660	2	US-09-903-562B-28	Sequence 28, Appl	241	309	9.9	649	3	US-10-063-646-132	Sequence 132, App
169	320	10.2	660	2	US-09-906-679A-28	Sequence 28, Appl	242	309	9.9	649	3	US-10-063-660-132	Sequence 384, App
170	320	10.2	660	2	US-09-973-424A-58	Sequence 58, Appl	243	309	9.9	649	3	US-10-207-916-384	Sequence 132, App
171	320	10.2	660	3	US-09-907-841-28	Sequence 28, Appl	244	309	9.9	649	3	US-10-063-647-132	Sequence 132, App
172	320	10.2	660	3	US-10-123-292-350	Sequence 350, App	245	309	9.9	649	3	US-10-063-661-132	Sequence 132, App

245	309	9.9	649	3	US-10-063-651-132	Sequence 132, App	319	301	9.6	448	2	US-09-520-781-32	Sequence 32, App1
247	309	9.9	649	3	US-10-063-530-132	Sequence 132, App	320	301	9.6	448	2	US-09-557-187-32	Sequence 32, App1
248	309	9.9	649	3	US-10-063-540-132	Sequence 132, App	321	301	9.6	448	2	US-09-991-053-32	Sequence 305, App
249	309	9.9	649	3	US-10-063-648-132	Sequence 132, App	322	298.5	9.5	649	2	US-09-188-930-305	Sequence 315, App
250	309	9.9	649	3	US-10-063-657-132	Sequence 132, App	323	298.5	9.5	649	2	US-09-312-283C-305	Sequence 292, App
251	309	9.9	649	3	US-10-063-702-132	Sequence 132, App	324	292.5	9.3	640	2	US-09-907-794A-292	Sequence 292, App
252	309	9.9	649	3	US-10-063-529-132	Sequence 132, App	325	292.5	9.3	640	2	US-09-905-125A-292	Sequence 292, App
253	309	9.9	649	3	US-10-063-644-132	Sequence 132, App	326	292.5	9.3	640	2	US-09-902-775A-292	Sequence 292, App
254	309	9.9	649	3	US-10-063-585-132	Sequence 132, App	327	292.5	9.3	640	2	US-09-906-700-292	Sequence 292, App
255	309	9.9	649	3	US-10-063-591A-132	Sequence 132, App	328	292.5	9.3	640	2	US-09-903-603A-292	Sequence 292, App
256	309	9.9	649	3	US-10-063-516-132	Sequence 132, App	329	292.5	9.3	640	2	US-09-904-920A-292	Sequence 292, App
257	309	9.9	649	3	US-10-063-532-132	Sequence 132, App	330	292.5	9.3	640	2	US-09-909-064-292	Sequence 292, App
258	309	9.9	649	3	US-10-063-654-132	Sequence 132, App	331	292.5	9.3	640	2	US-09-905-381A-292	Sequence 292, App
259	309	9.9	649	3	US-10-063-582-132	Sequence 132, App	332	292.5	9.3	640	2	US-09-906-618-292	Sequence 292, App
260	309	9.9	649	3	US-10-063-524-132	Sequence 132, App	333	292.5	9.3	640	2	US-09-906-646-292	Sequence 292, App
261	309	9.9	649	3	US-10-972-317-132	Sequence 132, App	334	292.5	9.3	640	2	US-09-904-462-292	Sequence 292, App
262	309	9.9	649	3	US-10-174-583-384	Sequence 384, App	335	292.5	9.3	640	2	US-09-902-736A-292	Sequence 292, App
263	309	9.9	649	3	US-10-063-551-132	Sequence 132, App	336	292.5	9.3	640	2	US-09-991-181-501	Sequence 501, App
264	309	9.9	649	3	US-10-063-650-132	Sequence 132, App	337	292.5	9.3	640	2	US-09-990-444-501	Sequence 501, App
265	309	9.9	649	3	US-10-063-600-132	Sequence 132, App	338	292.5	9.3	640	2	US-09-906-722A-292	Sequence 292, App
266	309	9.9	649	3	US-10-063-592A-132	Sequence 132, App	339	292.5	9.3	640	2	US-09-997-333-501	Sequence 501, App
267	309	9.9	649	3	US-10-063-705-132	Sequence 132, App	340	292.5	9.3	640	2	US-09-992-598-501	Sequence 501, App
268	309	9.9	649	3	US-10-063-598-132	Sequence 132, App	341	292.5	9.3	640	2	US-09-905-449-292	Sequence 292, App
269	309	9.9	649	3	US-10-063-554-132	Sequence 132, App	342	292.5	9.3	640	2	US-09-903-562B-292	Sequence 292, App
270	309	9.9	649	3	US-10-063-597-132	Sequence 132, App	343	292.5	9.3	640	2	US-09-989-735-501	Sequence 501, App
271	309	9.9	649	3	US-10-063-600-132	Sequence 132, App	344	292.5	9.3	640	3	US-09-906-679A-292	Sequence 292, App
272	309	9.9	649	3	US-10-063-652A-132	Sequence 132, App	345	292.5	9.3	640	3	US-09-989-726-501	Sequence 501, App
273	309	9.9	649	3	US-10-063-602-132	Sequence 132, App	346	292.5	9.3	640	3	US-09-997-514-501	Sequence 501, App
274	309	9.9	649	3	US-10-063-560-132	Sequence 132, App	347	292.5	9.3	640	3	US-09-989-728-501	Sequence 501, App
275	309	9.9	649	3	US-10-063-517-132	Sequence 132, App	348	292.5	9.3	640	3	US-09-907-841-292	Sequence 292, App
276	309	9.9	649	3	US-10-063-548-132	Sequence 132, App	349	292.5	9.3	640	3	US-09-997-349-501	Sequence 501, App
277	309	9.9	649	3	US-10-063-553-132	Sequence 132, App	350	292.5	9.3	640	3	US-09-997-653-501	Sequence 501, App
278	309	9.9	649	3	US-10-063-653A-132	Sequence 132, App	351	292.5	9.3	640	3	US-09-989-293A-501	Sequence 501, App
279	309	9.9	649	3	US-10-063-595-132	Sequence 132, App	352	292.5	9.3	640	3	US-09-989-732-501	Sequence 501, App
280	309	9.9	649	3	US-10-063-587-132	Sequence 132, App	353	292.5	9.3	640	3	US-09-990-441-501	Sequence 501, App
281	309	9.9	649	3	US-10-063-586-132	Sequence 132, App	354	292.5	9.3	640	3	US-10-123-292-368	Sequence 368, App
282	309	9.9	649	3	US-10-187-745-384	Sequence 384, App	355	292.5	9.3	640	3	US-09-989-328-501	Sequence 501, App
283	309	9.9	649	3	US-10-223-090-274	Sequence 274, App	356	292.5	9.3	640	3	US-09-989-724-501	Sequence 501, App
284	308	9.8	649	2	US-09-689-486-57	Sequence 57, App1	357	292.5	9.3	640	3	US-09-989-733-501	Sequence 501, App
285	308	9.8	649	2	US-09-973-424A-57	Sequence 57, App1	358	292.5	9.3	640	3	US-09-906-838B-292	Sequence 292, App
286	307.5	9.8	674	2	US-09-949-016-7204	Sequence 7204, App	359	292.5	9.3	640	3	US-09-909-320-292	Sequence 292, App
287	307.5	9.8	674	2	US-09-689-486-7	Sequence 7, App1	360	292.5	9.3	640	3	US-09-993-583-501	Sequence 501, App
288	307.5	9.8	674	2	US-09-973-424A-7	Sequence 7, App1	361	292.5	9.3	640	3	US-10-152-398-368	Sequence 368, App
289	307.5	9.8	674	3	US-10-123-292-36	Sequence 36, App1	362	292.5	9.3	640	3	US-09-989-279-501	Sequence 501, App
290	307.5	9.8	674	3	US-10-152-398-36	Sequence 36, App1	363	292.5	9.3	640	3	US-10-123-907-368	Sequence 368, App
291	307.5	9.8	674	3	US-10-123-907-36	Sequence 36, App1	364	292.5	9.3	640	3	US-10-147-512-368	Sequence 368, App
292	307.5	9.8	674	3	US-10-147-512-36	Sequence 36, App1	365	292.5	9.3	640	3	US-09-907-942-292	Sequence 292, App
293	307.5	9.8	674	3	US-10-147-485-36	Sequence 36, App1	366	292.5	9.3	640	3	US-09-906-815C-292	Sequence 292, App
294	307.5	9.8	674	3	US-10-124-814-36	Sequence 36, App1	367	292.5	9.3	640	3	US-10-147-485-368	Sequence 368, App
295	307.5	9.8	674	3	US-10-124-822-36	Sequence 36, App1	368	292.5	9.3	640	3	US-09-991-157-501	Sequence 501, App
296	307.5	9.8	674	3	US-10-131-833A-36	Sequence 36, App1	369	292.5	9.3	640	3	US-10-124-814-368	Sequence 368, App
297	307.5	9.8	674	3	US-10-142-419-36	Sequence 36, App1	370	292.5	9.3	640	3	US-10-124-822-368	Sequence 368, App
298	307.5	9.8	674	3	US-10-152-375-36	Sequence 36, App1	371	292.5	9.3	640	3	US-09-990-439-501	Sequence 501, App
299	307.5	9.8	674	3	US-10-131-818A-36	Sequence 36, App1	372	292.5	9.3	640	3	US-09-997-641-501	Sequence 501, App
300	307.5	9.8	674	3	US-10-145-873-36	Sequence 36, App1	373	292.5	9.3	640	3	US-09-997-384-501	Sequence 501, App
301	307.5	9.8	674	3	US-10-152-395-36	Sequence 36, App1	374	292.5	9.3	640	3	US-10-131-833A-368	Sequence 368, App
302	307.5	9.8	674	3	US-10-131-822A-36	Sequence 36, App1	375	292.5	9.3	640	3	US-09-903-749A-292	Sequence 292, App
303	307.5	9.8	674	3	US-10-142-419-36	Sequence 36, App1	376	292.5	9.3	640	3	US-09-904-532B-292	Sequence 292, App
304	307.5	9.8	674	3	US-10-128-694A-36	Sequence 36, App1	377	292.5	9.3	640	3	US-10-142-419-368	Sequence 368, App
305	307.5	9.8	674	3	US-10-123-213-36	Sequence 36, App1	378	292.5	9.3	640	3	US-09-989-730-501	Sequence 501, App
306	307.5	9.8	674	3	US-10-123-909-36	Sequence 36, App1	379	292.5	9.3	640	3	US-10-152-375-368	Sequence 368, App
307	307.5	9.8	674	3	US-10-131-826A-36	Sequence 36, App1	380	292.5	9.3	640	3	US-09-997-585-501	Sequence 501, App
308	307.5	9.8	674	3	US-10-147-513-36	Sequence 36, App1	381	292.5	9.3	640	3	US-10-131-818A-368	Sequence 368, App
309	307.5	9.8	674	3	US-10-121-043-36	Sequence 36, App1	382	292.5	9.3	640	3	US-09-905-075-292	Sequence 292, App
310	307.5	9.8	674	3	US-10-139-980-36	Sequence 36, App1	383	292.5	9.3	640	3	US-10-145-873-368	Sequence 368, App
311	305.5	9.7	664	2	US-09-973-424A-68	Sequence 68, App1	384	292.5	9.3	640	3	US-10-152-395-368	Sequence 368, App
312	302.5	9.6	420	3	US-10-735-256-2	Sequence 2, App1	385	292.5	9.3	640	3	US-10-131-822A-368	Sequence 368, App
313	302	9.6	605	1	US-08-190-802A-49	Sequence 49, App1	386	292.5	9.3	640	3	US-10-142-763-368	Sequence 368, App
314	302	9.6	605	2	US-08-477-346-49	Sequence 49, App1	387	292.5	9.3	640	3	US-10-128-694A-368	Sequence 368, App
315	302	9.6	605	2	US-08-473-089-49	Sequence 49, App1	388	292.5	9.3	640	3	US-09-997-601-501	Sequence 501, App
316	302	9.6	605	2	US-08-487-072A-49	Sequence 49, App1	389	292.5	9.3	640	3	US-10-123-213-368	Sequence 368, App
317	302	9.6	605	2	US-09-538-092-1087	Sequence 1087, App	390	292.5	9.3	640	3	US-10-123-909-368	Sequence 368, App
318	302	9.6	623	2	US-09-949-016-10995	Sequence 10995, App	391	292.5	9.3	640	3	US-10-131-826A-368	Sequence 368, App

392	292.5	9.3	640	3	US-09-903-640A-292	Sequence 282, App	465	271.5	8.7	353	2	US-08-986-485-6	Sequence 6, Appli
393	292.5	9.3	640	3	US-10-448-580-292	Sequence 282, App	466	271.5	8.7	1504	2	US-10-037-417-98	Sequence 98, Appl
394	292.5	9.3	640	3	US-10-147-513-368	Sequence 368, App	467	271	8.6	473	2	US-09-949-016-8448	Sequence 8448, Ap
395	292.5	9.3	640	3	US-10-121-043-368	Sequence 368, App	468	271	8.6	473	2	US-09-999-833A-400	Sequence 400, App
396	292.5	9.3	640	3	US-10-963-467-392	Sequence 392, App	469	271	8.6	473	2	US-10-020-445A-400	Sequence 400, App
397	292.5	9.3	640	3	US-10-448-923-292	Sequence 282, App	470	271	8.6	473	2	US-09-978-189-400	Sequence 400, App
398	292.5	9.3	640	3	US-09-997-666-501	Sequence 501, App	471	271	8.6	473	2	US-10-017-085A-400	Sequence 400, App
399	292.5	9.3	640	3	US-10-139-980-368	Sequence 368, App	472	271	8.6	473	3	US-10-145-129A-400	Sequence 400, App
400	287.5	9.2	713	2	US-09-907-794A-245	Sequence 245, App	473	271	8.6	473	3	US-10-013-929A-400	Sequence 400, App
401	287.5	9.2	713	2	US-09-905-125A-245	Sequence 245, App	474	271	8.6	473	3	US-10-013-917A-400	Sequence 400, App
402	287.5	9.2	713	2	US-09-902-775A-245	Sequence 245, App	475	271	8.6	473	3	US-10-013-925A-400	Sequence 400, App
403	287.5	9.2	713	2	US-09-906-700-245	Sequence 245, App	476	271	8.6	473	3	US-10-123-292-382	Sequence 382, App
404	287.5	9.2	713	2	US-09-903-603A-245	Sequence 245, App	477	271	8.6	473	3	US-10-162-521A-400	Sequence 400, App
405	287.5	9.2	713	2	US-09-904-920A-245	Sequence 245, App	478	271	8.6	473	3	US-10-145-016A-400	Sequence 400, App
406	287.5	9.2	713	2	US-09-909-064-245	Sequence 245, App	479	271	8.6	473	3	US-10-013-926A-400	Sequence 400, App
407	287.5	9.2	713	2	US-09-905-381A-245	Sequence 245, App	480	271	8.6	473	3	US-10-152-398-382	Sequence 382, App
408	287.5	9.2	713	2	US-09-906-618-245	Sequence 245, App	481	271	8.6	473	3	US-10-162-522A-400	Sequence 400, App
409	287.5	9.2	713	2	US-09-906-646-245	Sequence 245, App	482	271	8.6	473	3	US-10-123-907-382	Sequence 382, App
410	287.5	9.2	713	2	US-09-904-462-245	Sequence 245, App	483	271	8.6	473	3	US-10-147-512-382	Sequence 382, App
411	287.5	9.2	713	2	US-09-902-736A-245	Sequence 245, App	484	271	8.6	473	3	US-10-147-485-382	Sequence 382, App
412	287.5	9.2	713	2	US-09-906-722A-245	Sequence 245, App	485	271	8.6	473	3	US-10-124-814-382	Sequence 382, App
413	287.5	9.2	713	2	US-09-905-449-245	Sequence 245, App	486	271	8.6	473	3	US-10-143-029A-400	Sequence 400, App
414	287.5	9.2	713	2	US-09-903-562B-245	Sequence 245, App	487	271	8.6	473	3	US-10-124-822-382	Sequence 382, App
415	287.5	9.2	713	2	US-09-906-679A-245	Sequence 245, App	488	271	8.6	473	3	US-10-165-247A-400	Sequence 400, App
416	287.5	9.2	713	3	US-09-907-841-245	Sequence 245, App	489	271	8.6	473	3	US-09-972-599A-2	Sequence 2, Appli
417	287.5	9.2	713	3	US-09-906-838B-245	Sequence 245, App	490	271	8.6	473	3	US-10-017-086A-400	Sequence 400, App
418	287.5	9.2	713	3	US-09-909-320-245	Sequence 245, App	491	271	8.6	473	3	US-10-271-078-6	Sequence 6, Appli
419	287.5	9.2	713	3	US-09-907-912-245	Sequence 245, App	492	271	8.6	473	3	US-10-271-078-7	Sequence 7, Appli
420	287.5	9.2	713	3	US-09-906-815C-245	Sequence 245, App	493	271	8.6	473	3	US-10-219-074-128	Sequence 128, App
421	287.5	9.2	713	3	US-09-903-749A-245	Sequence 245, App	494	271	8.6	473	3	US-10-227-873-128	Sequence 128, App
422	287.5	9.2	713	3	US-09-904-532B-245	Sequence 245, App	495	271	8.6	473	3	US-09-999-832A-400	Sequence 400, App
423	287.5	9.2	713	3	US-09-905-075-245	Sequence 245, App	496	271	8.6	473	3	US-10-131-833A-382	Sequence 382, App
424	287.5	9.2	713	3	US-09-903-640A-245	Sequence 245, App	497	271	8.6	473	3	US-10-218-849-128	Sequence 128, App
425	287.5	9.2	713	3	US-10-448-580-245	Sequence 245, App	498	271	8.6	473	3	US-10-142-419-382	Sequence 382, App
426	287.5	9.2	713	3	US-10-963-467-245	Sequence 245, App	499	271	8.6	473	3	US-10-216-168-128	Sequence 128, App
427	287.5	9.2	713	3	US-10-448-923-245	Sequence 245, App	500	271	8.6	473	3	US-10-152-375-382	Sequence 382, App
428	284.5	9.1	745	2	US-10-104-047-2955	Sequence 2955, Ap	501	271	8.6	473	3	US-10-143-031A-400	Sequence 400, App
429	283.5	9.0	713	3	US-10-193-477-41	Sequence 41, Appl	502	271	8.6	473	3	US-10-131-818A-382	Sequence 382, App
430	282.5	9.0	390	3	US-10-735-256-8	Sequence 8, Appli	503	271	8.6	473	3	US-10-013-923A-400	Sequence 400, App
431	282.5	9.0	745	2	US-10-104-047-2960	Sequence 2960, Ap	504	271	8.6	473	3	US-10-735-256-5	Sequence 5, Appli
432	282.5	9.0	745	3	US-10-123-292-68	Sequence 68, Appl	505	271	8.6	473	3	US-10-013-827A-400	Sequence 400, App
433	282.5	9.0	745	3	US-10-152-398-68	Sequence 68, Appl	506	271	8.6	473	3	US-10-145-873-382	Sequence 382, App
434	282.5	9.0	745	3	US-10-123-907-68	Sequence 68, Appl	507	271	8.6	473	3	US-10-152-395-382	Sequence 382, App
435	282.5	9.0	745	3	US-10-147-512-68	Sequence 68, Appl	508	271	8.6	473	3	US-10-131-822A-382	Sequence 382, App
436	282.5	9.0	745	3	US-10-147-485-68	Sequence 68, Appl	509	271	8.6	473	3	US-10-142-763-382	Sequence 382, App
437	282.5	9.0	745	3	US-10-124-814-68	Sequence 68, Appl	510	271	8.6	473	3	US-10-128-694A-382	Sequence 382, App
438	282.5	9.0	745	3	US-10-124-822-68	Sequence 68, Appl	511	271	8.6	473	3	US-10-123-213-382	Sequence 382, App
439	282.5	9.0	745	3	US-10-131-833A-68	Sequence 68, Appl	512	271	8.6	473	3	US-10-123-909-382	Sequence 382, App
440	282.5	9.0	745	3	US-10-142-419-68	Sequence 68, Appl	513	271	8.6	473	3	US-10-145-087A-400	Sequence 400, App
441	282.5	9.0	745	3	US-10-152-375-68	Sequence 68, Appl	514	271	8.6	473	3	US-09-978-564A-400	Sequence 400, App
442	282.5	9.0	745	3	US-10-131-818A-68	Sequence 68, Appl	515	271	8.6	473	3	US-09-978-375A-400	Sequence 400, App
443	282.5	9.0	745	3	US-10-145-873-68	Sequence 68, Appl	516	271	8.6	473	3	US-10-165-353A-400	Sequence 400, App
444	282.5	9.0	745	3	US-10-152-395-68	Sequence 68, Appl	517	271	8.6	473	3	US-10-143-030A-400	Sequence 400, App
445	282.5	9.0	745	3	US-10-131-822A-68	Sequence 68, Appl	518	271	8.6	473	3	US-10-131-826A-382	Sequence 382, App
446	282.5	9.0	745	3	US-10-142-763-68	Sequence 68, Appl	519	271	8.6	473	3	US-10-145-089A-400	Sequence 400, App
447	282.5	9.0	745	3	US-10-128-694A-68	Sequence 68, Appl	520	271	8.6	473	3	US-10-170-481A-400	Sequence 400, App
448	282.5	9.0	745	3	US-10-123-213-68	Sequence 68, Appl	521	271	8.6	473	3	US-10-147-513-382	Sequence 382, App
449	282.5	9.0	745	3	US-10-123-909-68	Sequence 68, Appl	522	271	8.6	473	3	US-10-121-043-382	Sequence 382, App
450	282.5	9.0	745	3	US-10-108-260A-3826	Sequence 3826, Ap	523	271	8.6	473	3	US-10-160-502A-400	Sequence 400, App
451	282.5	9.0	745	3	US-10-131-826A-68	Sequence 68, Appl	524	271	8.6	473	3	US-10-139-980-382	Sequence 382, App
452	282.5	9.0	745	3	US-10-147-513-68	Sequence 68, Appl	525	270	8.6	590	3	US-10-193-477-6	Sequence 6, Appli
453	282.5	9.0	745	3	US-10-121-043-68	Sequence 68, Appl	526	259	8.3	610	1	US-07-821-717B-6	Sequence 6, Appli
454	282.5	9.0	745	3	US-10-119-980-68	Sequence 68, Appl	527	259	8.3	610	1	US-08-119-262B-6	Sequence 11, Appl
455	281.5	9.0	603	1	US-08-190-802A-50	Sequence 50, Appl	528	259	8.3	610	1	US-08-135-929A-11	Sequence 11, Appl
456	281.5	9.0	603	2	US-08-477-346-50	Sequence 50, Appl	529	259	8.3	610	1	US-08-234-265A-11	Sequence 2, Appli
457	281.5	9.0	603	2	US-08-473-089-50	Sequence 50, Appl	530	258	8.2	1523	2	US-09-182-024A-2	Sequence 2, Appli
458	281.5	9.0	603	2	US-08-487-072A-50	Sequence 50, Appl	531	258	8.2	1523	2	US-10-012-231A-198	Sequence 198, App
459	276	8.8	473	3	US-10-775-204-1826	Sequence 1826, Ap	532	258	8.2	1523	2	US-10-015-389A-198	Sequence 198, App
460	276	8.8	473	3	US-10-775-204-1827	Sequence 1827, Ap	533	258	8.2	1523	2	US-10-006-768A-198	Sequence 198, App
461	276	8.8	473	3	US-11-429-373-1826	Sequence 1826, Ap	534	258	8.2	1523	2	US-10-005-671A-198	Sequence 198, App
462	276	8.8	473	3	US-10-429-373-1827	Sequence 1827, Ap	535	258	8.2	1523	2	US-10-015-393A-198	Sequence 198, App
463	273.5	8.7	593	3	US-10-193-477-154	Sequence 154, App	536	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, App
464	272	8.7	473	3	US-09-796-858A-34	Sequence 34, Appl	537	258	8.2	1523	2	US-10-006-041A-198	Sequence 198, App

538	258	8.2	1523	2	US-10-012-064A-198	Sequence 198, App	611	247.5	7.9	470	3	US-10-223-081-58	Sequence 58, Appl
539	258	8.2	1523	2	US-10-015-392A-198	Sequence 198, App	612	247.5	7.9	470	3	US-10-223-082-58	Sequence 58, Appl
540	258	8.2	1523	3	US-10-011-795B-198	Sequence 198, App	613	247.5	7.9	470	3	US-10-223-082-58	Sequence 58, Appl
541	258	8.2	1523	3	US-10-015-386A-198	Sequence 198, App	614	247.5	7.9	470	3	US-10-223-084-58	Sequence 58, Appl
542	258	8.2	1523	3	US-10-012-121A-198	Sequence 198, App	615	247.5	7.9	470	3	US-10-223-090-58	Sequence 2, Appli
543	258	8.2	1523	3	US-10-006-485A-198	Sequence 198, App	616	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appli
544	258	8.2	1523	3	US-10-006-746A-198	Sequence 198, App	617	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appli
545	258	8.2	1523	3	US-10-012-752A-198	Sequence 198, App	618	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appli
546	258	8.2	1523	3	US-10-017-253A-198	Sequence 198, App	619	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appli
547	258	8.2	1523	3	US-10-015-519A-198	Sequence 198, App	620	247.5	7.9	1529	3	US-10-188-495-67	Sequence 67, Appl
548	258	8.2	1523	3	US-10-015-715A-198	Sequence 198, App	621	247.5	7.9	1529	3	US-09-766-511B-29	Sequence 29, Appl
549	258	8.2	1523	3	US-10-007-236A-198	Sequence 198, App	622	246.5	7.9	1529	3	US-09-312-283C-396	Sequence 396, App
550	258	8.2	1523	3	US-10-012-149A-198	Sequence 198, App	623	244	7.8	567	3	US-10-080-334-228	Sequence 228, App
551	258	8.2	1523	3	US-10-007-194A-198	Sequence 198, App	624	244	7.8	708	2	US-09-131-648-2	Sequence 2, Appli
552	258	8.2	1523	3	US-10-013-910A-198	Sequence 198, App	625	244	7.8	708	2	US-09-907-794A-69	Sequence 69, Appl
553	258	8.2	1523	3	US-10-006-117A-198	Sequence 198, App	626	244	7.8	708	2	US-09-905-125A-69	Sequence 69, Appl
554	258	8.2	1523	3	US-10-015-480A-198	Sequence 198, App	627	244	7.8	708	2	US-09-902-775A-69	Sequence 69, Appl
555	258	8.2	1523	3	US-10-006-172A-198	Sequence 198, App	628	244	7.8	708	2	US-09-906-700-69	Sequence 69, Appl
556	258	8.2	1523	3	US-10-015-395A-198	Sequence 198, App	629	244	7.8	708	2	US-09-903-603A-69	Sequence 69, Appl
557	258	8.2	1523	3	US-10-183-001-290	Sequence 290, App	630	244	7.8	708	2	US-09-904-920A-69	Sequence 69, Appl
558	258	8.2	1523	3	US-10-015-610A-198	Sequence 198, App	631	244	7.8	708	2	US-09-909-064-69	Sequence 69, Appl
559	258	8.2	1523	3	US-10-180-998-290	Sequence 290, App	632	244	7.8	708	2	US-09-905-381A-69	Sequence 69, Appl
560	258	8.2	1523	3	US-10-201-769-290	Sequence 290, App	633	244	7.8	708	2	US-09-906-618-69	Sequence 69, Appl
561	258	8.2	1523	3	US-10-006-130A-198	Sequence 198, App	634	244	7.8	708	2	US-09-906-646-69	Sequence 69, Appl
562	258	8.2	1523	3	US-10-174-576-290	Sequence 290, App	635	244	7.8	708	2	US-09-904-462-69	Sequence 69, Appl
563	258	8.2	1523	3	US-10-174-581-290	Sequence 290, App	636	244	7.8	708	2	US-09-902-736A-69	Sequence 69, Appl
564	258	8.2	1523	3	US-10-015-869A-198	Sequence 198, App	637	244	7.8	708	2	US-09-906-722A-69	Sequence 69, Appl
565	258	8.2	1523	3	US-10-207-916-290	Sequence 290, App	638	244	7.8	708	2	US-09-905-449-69	Sequence 69, Appl
566	258	8.2	1523	3	US-10-174-583-290	Sequence 290, App	639	244	7.8	708	2	US-09-903-562B-69	Sequence 69, Appl
567	258	8.2	1523	3	US-10-187-745-290	Sequence 290, App	640	244	7.8	708	2	US-09-906-679A-69	Sequence 69, Appl
568	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appli	641	244	7.8	708	3	US-09-907-841-69	Sequence 69, Appl
569	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appli	642	244	7.8	708	3	US-10-123-292-298	Sequence 298, App
570	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appli	643	244	7.8	708	3	US-09-906-838B-69	Sequence 69, Appl
571	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appli	644	244	7.8	708	3	US-09-909-320-69	Sequence 69, Appl
572	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appli	645	244	7.8	708	3	US-10-152-398-298	Sequence 298, App
573	255.5	8.1	1480	5	FC7-US91-09053-2	Sequence 2, Appli	646	244	7.8	708	3	US-10-123-907-298	Sequence 298, App
574	253	8.1	567	2	US-10-037-417-106	Sequence 106, App	647	244	7.8	708	3	US-10-147-512-298	Sequence 298, App
575	252	8.0	566	2	US-09-775-803-12	Sequence 12, Appl	648	244	7.8	708	3	US-09-907-942-69	Sequence 69, Appl
576	252	8.0	567	2	US-10-037-417-105	Sequence 105, App	649	244	7.8	708	3	US-09-906-815C-69	Sequence 69, Appl
577	251	8.0	473	3	US-09-796-858A-36	Sequence 36, Appl	650	244	7.8	708	3	US-10-147-485-298	Sequence 298, App
578	251	8.0	473	3	US-09-972-599A-4	Sequence 4, Appli	651	244	7.8	708	3	US-10-124-814-298	Sequence 298, App
579	251	8.0	473	3	US-10-271-078-8	Sequence 8, Appli	652	244	7.8	708	3	US-10-124-822-298	Sequence 298, App
580	251	8.0	473	3	US-10-735-256-17	Sequence 17, Appl	653	244	7.8	708	3	US-10-131-833A-298	Sequence 298, App
581	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl	654	244	7.8	708	3	US-09-903-749A-69	Sequence 69, Appl
582	251	8.0	622	3	US-10-123-292-180	Sequence 180, App	655	244	7.8	708	3	US-09-904-532B-69	Sequence 69, Appl
583	251	8.0	622	3	US-10-152-398-180	Sequence 180, App	656	244	7.8	708	3	US-10-142-419-298	Sequence 298, App
584	251	8.0	622	3	US-10-123-907-180	Sequence 180, App	657	244	7.8	708	3	US-10-152-375-298	Sequence 298, App
585	251	8.0	622	3	US-10-147-512-180	Sequence 180, App	658	244	7.8	708	3	US-10-131-818A-298	Sequence 298, App
586	251	8.0	622	3	US-10-147-485-180	Sequence 180, App	659	244	7.8	708	3	US-09-905-075-69	Sequence 69, Appl
587	251	8.0	622	3	US-10-124-814-180	Sequence 180, App	660	244	7.8	708	3	US-10-145-873-298	Sequence 298, App
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589	251	8.0	622	3	US-10-424-233-5	Sequence 5, Appli	662	244	7.8	708	3	US-10-414-378-64	Sequence 64, Appl
590	251	8.0	622	3	US-10-424-233-8	Sequence 8, Appli	663	244	7.8	708	3	US-10-131-822A-298	Sequence 298, App
591	251	8.0	622	3	US-10-131-833A-180	Sequence 180, App	664	244	7.8	708	3	US-10-142-763-298	Sequence 298, App
592	251	8.0	622	3	US-10-142-419-180	Sequence 180, App	665	244	7.8	708	3	US-10-128-694A-298	Sequence 298, App
593	251	8.0	622	3	US-09-766-511B-23	Sequence 23, Appl	666	244	7.8	708	3	US-10-123-213-298	Sequence 298, App
594	251	8.0	622	3	US-10-152-375-180	Sequence 180, App	667	244	7.8	708	3	US-10-123-909-298	Sequence 298, App
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598	251	8.0	622	3	US-10-131-822A-180	Sequence 180, App	671	244	7.8	708	3	US-10-147-513-298	Sequence 298, App
599	251	8.0	622	3	US-10-142-763-180	Sequence 180, App	672	244	7.8	708	3	US-10-121-043-298	Sequence 298, App
600	251	8.0	622	3	US-10-128-694A-180	Sequence 180, App	673	244	7.8	708	3	US-10-963-467-69	Sequence 69, Appl
601	251	8.0	622	3	US-10-123-213-180	Sequence 180, App	674	244	7.8	708	3	US-10-448-923-69	Sequence 69, Appl
602	251	8.0	622	3	US-10-123-909-180	Sequence 180, App	675	244	7.8	708	3	US-10-139-980-298	Sequence 298, App
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609	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appli	682	240	7.7	560	2	US-08-592-500-2	Sequence 2, Appli
610	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, App	683	240	7.7	560	2	US-08-195-006-2	Sequence 2, Appli

684	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appli	757	220.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appli
685	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appli	758	220.5	7.0	841	3	US-09-949-192-27	Sequence 27, Appli
686	240	7.7	560	5	PCT-US94-0764A-2	Sequence 2, Appli	759	218.5	7.0	359	3	US-09-949-016-9732	Sequence 9732, Ap
687	237.5	7.6	391	3	US-10-080-334-227	Sequence 227, App	760	217.5	6.9	291	3	US-09-876-997-309	Sequence 309, App
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689	237	7.6	578	3	US-10-080-334-226	Sequence 226, App	762	217.5	6.9	837	2	US-09-964-956-5	Sequence 5, Appli
690	236.5	7.5	222	5	PCT-US91-09055-3	Sequence 3, Appli	763	216.5	6.9	535	3	US-10-021-698A-126	Sequence 126, App
691	236.5	7.5	231	2	US-08-986-485-7	Sequence 7, Appli	764	214.5	6.8	255	2	US-09-893-737-232	Sequence 232, App
692	231	7.4	570	3	US-10-424-233-14	Sequence 14, Appl	765	214.5	6.8	716	3	US-10-123-292-512	Sequence 512, App
693	230.5	7.4	544	2	US-10-068-426-1	Sequence 1, Appli	766	214.5	6.8	716	3	US-10-152-398-512	Sequence 512, App
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697	229	7.3	581	3	US-10-080-334-76	Sequence 76, Appl	770	214.5	6.8	716	3	US-10-124-814-512	Sequence 512, App
698	229	7.3	581	3	US-10-080-334-225	Sequence 225, App	771	214.5	6.8	716	3	US-10-124-822-512	Sequence 512, App
699	229	7.3	597	3	US-10-424-233-9	Sequence 9, Appli	772	214.5	6.8	716	3	US-10-223-081-222	Sequence 222, App
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701	227.5	7.3	719	3	US-10-108-260A-3841	Sequence 3841, Ap	774	214.5	6.8	716	3	US-10-227-873-190	Sequence 190, App
702	227	7.2	568	2	US-09-673-245-14	Sequence 14, Appl	775	214.5	6.8	716	3	US-10-223-087-222	Sequence 222, App
703	226.5	7.2	291	3	US-09-876-997-304	Sequence 304, App	776	214.5	6.8	716	3	US-10-131-833A-512	Sequence 512, App
704	226.5	7.2	544	2	US-10-068-426-3	Sequence 3, Appli	777	214.5	6.8	716	3	US-10-218-849-190	Sequence 190, App
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718	226	7.2	283	3	US-09-972-599A-55	Sequence 55, Appl	791	214.5	6.8	716	3	US-10-131-826A-512	Sequence 512, App
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722	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appli	795	214.5	6.8	716	3	US-10-223-090-222	Sequence 222, App
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724	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appli	797	214	6.8	2828	3	US-09-522-699A-2	Sequence 2, Appli
725	224.5	7.2	281	3	US-10-123-292-54	Sequence 54, Appl	798	212	6.8	531	2	US-10-068-426-6	Sequence 6, Appli
726	224.5	7.2	281	3	US-10-152-398-54	Sequence 54, Appl	799	212	6.8	531	2	US-10-382-758-6	Sequence 6, Appli
727	224.5	7.2	281	3	US-10-123-907-54	Sequence 54, Appl	800	211	6.7	513	2	US-10-012-231A-385	Sequence 385, App
728	224.5	7.2	281	3	US-10-147-512-54	Sequence 54, Appl	801	211	6.7	513	2	US-10-015-389A-385	Sequence 385, App
729	224.5	7.2	281	3	US-10-147-485-54	Sequence 54, Appl	802	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App
730	224.5	7.2	281	3	US-10-124-814-54	Sequence 54, Appl	803	211	6.7	513	2	US-10-015-671A-385	Sequence 385, App
731	224.5	7.2	281	3	US-10-124-822-54	Sequence 54, Appl	804	211	6.7	513	2	US-10-015-393A-385	Sequence 385, App
732	224.5	7.2	281	3	US-10-131-833A-54	Sequence 54, Appl	805	211	6.7	513	2	US-10-011-833A-385	Sequence 385, App
733	224.5	7.2	281	3	US-10-142-419-54	Sequence 54, Appl	806	211	6.7	513	2	US-10-006-041A-385	Sequence 385, App
734	224.5	7.2	281	3	US-10-152-375-54	Sequence 54, Appl	807	211	6.7	513	2	US-10-012-064A-385	Sequence 385, App
735	224.5	7.2	281	3	US-10-131-818A-54	Sequence 54, Appl	808	211	6.7	513	2	US-10-015-392A-385	Sequence 385, App
736	224.5	7.2	281	3	US-10-145-873-54	Sequence 54, Appl	809	211	6.7	513	3	US-10-011-795B-385	Sequence 385, App
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738	224.5	7.2	281	3	US-10-131-822A-54	Sequence 54, Appl	811	211	6.7	513	3	US-10-012-121A-385	Sequence 385, App
739	224.5	7.2	281	3	US-10-142-763-54	Sequence 54, Appl	812	211	6.7	513	3	US-10-006-485A-385	Sequence 385, App
740	224.5	7.2	281	3	US-10-128-694A-54	Sequence 54, Appl	813	211	6.7	513	3	US-10-006-746A-385	Sequence 385, App
741	224.5	7.2	281	3	US-10-123-213-54	Sequence 54, Appl	814	211	6.7	513	3	US-10-012-752A-385	Sequence 385, App
742	224.5	7.2	281	3	US-10-123-909-54	Sequence 54, Appl	815	211	6.7	513	3	US-10-017-253A-385	Sequence 385, App
743	224.5	7.2	281	3	US-10-131-826A-54	Sequence 54, Appl	816	211	6.7	513	3	US-10-015-519A-385	Sequence 385, App
744	224.5	7.2	281	3	US-10-147-513-54	Sequence 54, Appl	817	211	6.7	513	3	US-10-015-715A-385	Sequence 385, App
745	224.5	7.2	281	3	US-10-121-043-54	Sequence 54, Appl	818	211	6.7	513	3	US-10-007-236A-385	Sequence 385, App
746	224.5	7.2	281	3	US-10-139-980-54	Sequence 54, Appl	819	211	6.7	513	3	US-10-012-149A-385	Sequence 385, App
747	222.5	7.1	536	2	US-09-538-092-992	Sequence 992, App	820	211	6.7	513	3	US-10-007-194A-385	Sequence 385, App
748	222	7.1	196	5	PCT-US91-09055-5	Sequence 5, Appli	821	211	6.7	513	3	US-10-123-292-536	Sequence 536, App
749	222	7.1	498	2	US-10-188-495-51	Sequence 51, Appl	822	211	6.7	513	3	US-10-013-910A-385	Sequence 385, App
750	222	7.1	498	3	US-10-424-233-7	Sequence 7, Appli	823	211	6.7	513	3	US-10-006-117A-385	Sequence 385, App
751	222	7.1	498	3	US-09-766-511B-26	Sequence 26, Appl	824	211	6.7	513	3	US-10-152-398-536	Sequence 536, App
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837	211	6.7	513	3	US-10-124-822-536	Sequence 536, App	910	210.5	6.7	4302	2	US-09-052-469-8	Sequence 8, Appli
838	211	6.7	513	3	US-10-063-741-124	Sequence 124, App	911	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appli
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840	211	6.7	513	3	US-10-131-833A-536	Sequence 536, App	913	210.5	6.7	4302	3	US-10-080-334-271	Sequence 271, App
841	211	6.7	513	3	US-10-142-419-536	Sequence 536, App	914	210.5	6.7	4302	3	US-10-080-334-272	Sequence 272, App
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843	211	6.7	513	3	US-10-152-375-536	Sequence 536, App	916	210	6.7	531	2	US-10-382-758-4	Sequence 4, Appli
844	211	6.7	513	3	US-10-131-818A-536	Sequence 536, App	917	209	6.7	353	2	US-10-012-231A-397	Sequence 397, App
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850	211	6.7	513	3	US-10-152-395-536	Sequence 536, App	923	209	6.7	353	2	US-10-006-041A-397	Sequence 397, App
851	211	6.7	513	3	US-10-063-703-124	Sequence 124, App	924	209	6.7	353	2	US-10-012-064A-397	Sequence 397, App
852	211	6.7	513	3	US-10-063-709-124	Sequence 124, App	925	209	6.7	353	2	US-10-015-392A-397	Sequence 397, App
853	211	6.7	513	3	US-10-063-581-124	Sequence 124, App	926	209	6.7	353	2	US-10-011-795B-397	Sequence 397, App
854	211	6.7	513	3	US-10-063-593-124	Sequence 124, App	927	209	6.7	353	3	US-10-015-386A-397	Sequence 397, App
855	211	6.7	513	3	US-10-131-822A-536	Sequence 536, App	928	209	6.7	353	3	US-10-012-121A-397	Sequence 397, App
856	211	6.7	513	3	US-10-142-763-536	Sequence 536, App	929	209	6.7	353	3	US-10-006-485A-397	Sequence 397, App
857	211	6.7	513	3	US-10-128-694A-536	Sequence 536, App	930	209	6.7	353	3	US-10-006-746A-397	Sequence 397, App
858	211	6.7	513	3	US-10-063-599-124	Sequence 124, App	931	209	6.7	353	3	US-10-012-752A-397	Sequence 397, App
859	211	6.7	513	3	US-10-063-646-124	Sequence 124, App	932	209	6.7	353	3	US-10-017-253A-397	Sequence 397, App
860	211	6.7	513	3	US-10-063-660-124	Sequence 124, App	933	209	6.7	353	3	US-10-015-519A-397	Sequence 397, App
861	211	6.7	513	3	US-10-063-647-124	Sequence 124, App	934	209	6.7	353	3	US-10-015-715A-397	Sequence 397, App
862	211	6.7	513	3	US-10-063-661-124	Sequence 124, App	935	209	6.7	353	3	US-10-007-236A-397	Sequence 397, App
863	211	6.7	513	3	US-10-123-213-536	Sequence 536, App	936	209	6.7	353	3	US-10-012-149A-397	Sequence 397, App
864	211	6.7	513	3	US-10-123-909-536	Sequence 536, App	937	209	6.7	353	3	US-10-007-194A-397	Sequence 397, App
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866	211	6.7	513	3	US-10-063-530-124	Sequence 124, App	939	209	6.7	353	3	US-10-006-117A-397	Sequence 397, App
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868	211	6.7	513	3	US-10-063-648-124	Sequence 124, App	941	209	6.7	353	3	US-10-006-172A-397	Sequence 397, App
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870	211	6.7	513	3	US-10-063-702-124	Sequence 124, App	943	209	6.7	353	3	US-10-015-610A-397	Sequence 397, App
871	211	6.7	513	3	US-10-063-529-124	Sequence 124, App	944	209	6.7	353	3	US-10-006-130A-397	Sequence 397, App
872	211	6.7	513	3	US-10-063-644-124	Sequence 124, App	945	209	6.7	353	3	US-10-015-869A-397	Sequence 397, App
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874	211	6.7	513	3	US-10-063-591A-124	Sequence 124, App	947	208.5	6.7	424	2	US-09-949-016-7950	Sequence 7950, Ap
875	211	6.7	513	3	US-10-063-516-124	Sequence 124, App	948	208.5	6.7	461	3	US-10-735-256-4	Sequence 4, Appli
876	211	6.7	513	3	US-10-063-532-124	Sequence 124, App	949	208.5	6.7	590	3	US-10-219-074-70	Sequence 70, Appl
877	211	6.7	513	3	US-10-063-654-124	Sequence 124, App	950	208.5	6.7	590	3	US-10-227-873-70	Sequence 2, Appli
878	211	6.7	513	3	US-10-131-826A-536	Sequence 536, App	951	208.5	6.7	590	3	US-10-424-233-2	Sequence 2, Appli
879	211	6.7	513	3	US-10-063-582-124	Sequence 124, App	952	208.5	6.7	590	3	US-10-218-849-70	Sequence 70, Appl
880	211	6.7	513	3	US-10-063-524-124	Sequence 124, App	953	208.5	6.7	590	3	US-10-216-168-70	Sequence 70, Appl
881	211	6.7	513	3	US-10-972-117-124	Sequence 124, App	954	207.5	6.6	415	2	US-09-935-430-659	Sequence 659, App
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883	211	6.7	513	3	US-10-063-650-124	Sequence 124, App	956	207.5	6.6	440	3	US-10-424-233-20	Sequence 20, Appl
884	211	6.7	513	3	US-10-147-513-536	Sequence 536, App	957	207.5	6.6	798	2	US-09-935-430-658	Sequence 658, App
885	211	6.7	513	3	US-10-063-523-124	Sequence 124, App	958	207.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl
886	211	6.7	513	3	US-10-121-043-536	Sequence 536, App	959	206.5	6.6	1101	2	US-08-986-485-2	Sequence 2, Appli
887	211	6.7	513	3	US-10-063-592A-124	Sequence 124, App	960	206	6.6	353	3	US-10-305-278-194	Sequence 194, App
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889	211	6.7	513	3	US-10-063-598-124	Sequence 124, App	962	206	6.6	428	3	US-10-123-292-292	Sequence 292, App
890	211	6.7	513	3	US-10-063-554-124	Sequence 124, App	963	206	6.6	428	3	US-10-152-398-292	Sequence 292, App
891	211	6.7	513	3	US-10-063-597-124	Sequence 124, App	964	206	6.6	428	3	US-10-123-907-292	Sequence 292, App
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893	211	6.7	513	3	US-10-063-652A-124	Sequence 124, App	966	206	6.6	428	3	US-10-147-485-292	Sequence 292, App
894	211	6.7	513	3	US-10-063-602-124	Sequence 124, App	967	206	6.6	428	3	US-10-124-814-292	Sequence 292, App
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977	206	6.6	428	3	US-10-128-694A-292	Sequence 292, App	1050	195	6.2	620	2	US-09-909-064-73	Sequence 73, Appl
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991	203.5	6.5	4303	2	US-10-080-334-274	Sequence 274, App	1064	195	6.2	620	3	US-10-152-398-324	Sequence 324, App
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993	201.5	6.4	606	3	US-10-193-477-4	Sequence 4, Appli	1066	195	6.2	620	3	US-10-147-512-324	Sequence 324, App
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1008	197.5	6.3	616	2	US-10-011-833A-24	Sequence 24, Appl	1081	195	6.2	620	3	US-10-131-822A-324	Sequence 324, App
1009	197.5	6.3	616	2	US-10-006-041A-24	Sequence 24, Appl	1082	195	6.2	620	3	US-10-142-763-324	Sequence 324, App
1010	197.5	6.3	616	2	US-10-012-064A-24	Sequence 24, Appl	1083	195	6.2	620	3	US-10-128-694A-324	Sequence 324, App
1011	197.5	6.3	616	2	US-10-015-392A-24	Sequence 24, Appl	1084	195	6.2	620	3	US-10-123-213-324	Sequence 324, App
1012	197.5	6.3	616	3	US-10-011-795B-24	Sequence 24, Appl	1085	195	6.2	620	3	US-10-123-909-324	Sequence 324, App
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1018	197.5	6.3	616	3	US-10-017-253A-24	Sequence 24, Appl	1091	195	6.2	620	3	US-10-963-467-73	Sequence 73, Appl
1019	197.5	6.3	616	3	US-10-015-519A-24	Sequence 24, Appl	1092	195	6.2	620	3	US-10-448-923-73	Sequence 73, Appl
1020	197.5	6.3	616	3	US-10-015-715A-24	Sequence 24, Appl	1093	195	6.2	620	3	US-10-139-980-324	Sequence 324, App
1021	197.5	6.3	616	3	US-10-007-236A-24	Sequence 24, Appl	1094	195	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap
1022	197.5	6.3	616	3	US-10-012-149A-24	Sequence 24, Appl	1095	195	6.2	832	2	US-09-935-430-660	Sequence 660, App
1023	197.5	6.3	616	3	US-10-007-194A-24	Sequence 24, Appl	1096	195	6.2	837	3	US-09-949-192-25	Sequence 25, Appl
1024	197.5	6.3	616	3	US-10-013-910A-24	Sequence 24, Appl	1097	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl
1025	197.5	6.3	616	3	US-10-006-117A-24	Sequence 24, Appl	1098	194.5	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap
1026	197.5	6.3	616	3	US-10-015-480A-24	Sequence 24, Appl	1099	194.5	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap
1027	197.5	6.3	616	3	US-10-006-72A-24	Sequence 24, Appl	1100	193.5	6.2	224	5	PCT-US91-09055-4	Sequence 4, Appli
1028	197.5	6.3	616	3	US-10-015-395A-24	Sequence 24, Appl	1101	193.5	6.2	542	2	US-10-037-417-97	Sequence 97, Appl
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1031	197.5	6.3	616	3	US-10-180-998-158	Sequence 158, App	1104	191.5	6.1	421	3	US-10-735-256-9	Sequence 9, Appli
1032	197.5	6.3	616	3	US-10-201-769-158	Sequence 158, App	1105	190	6.1	1059	2	US-09-907-794A-290	Sequence 290, App
1033	197.5	6.3	616	3	US-10-006-130A-24	Sequence 24, Appl	1106	190	6.1	1059	2	US-09-905-125A-290	Sequence 290, App
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1036	197.5	6.3	616	3	US-10-015-869A-24	Sequence 24, Appl	1109	190	6.1	1059	2	US-09-903-603A-290	Sequence 290, App
1037	197.5	6.3	616	3	US-10-207-916-158	Sequence 158, App	1110	190	6.1	1059	2	US-09-904-920A-290	Sequence 290, App
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1039	197.5	6.3	616	3	US-10-187-745-158	Sequence 158, App	1112	190	6.1	1059	2	US-09-905-381A-290	Sequence 290, App
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1043	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl	1116	190	6.1	1059	2	US-09-902-736A-290	Sequence 290, App
1044	195	6.2	620	2	US-09-907-794A-73	Sequence 73, Appl	1117	190	6.1	1059	2	US-09-906-722A-290	Sequence 290, App
1045	195	6.2	620	2	US-09-905-125A-73	Sequence 73, Appl	1118	190	6.1	1059	2	US-09-905-449-290	Sequence 290, App
1046	195	6.2	620	2	US-09-902-752A-73	Sequence 73, Appl	1119	190	6.1	1059	2	US-09-903-562B-290	Sequence 290, App
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1124	190	6.1	1059	3	US-09-907-942-290	Sequence 290, App	1197	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap
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1126	190	6.1	1059	3	US-09-903-749A-290	Sequence 290, App	1199	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A
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1132	190	6.1	1059	3	US-10-448-923-290	Sequence 290, App	1205	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli
1133	190	6.1	1059	3	US-09-907-794A-294	Sequence 294, App	1206	182.5	5.8	379	2	US-09-945-584-2	Sequence 2, Appli
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1135	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App	1208	182.5	5.8	379	2	US-09-945-587-2	Sequence 2, Appli
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1137	190	6.1	1119	2	US-09-903-603A-294	Sequence 294, App	1210	182.5	5.8	379	3	US-10-123-292-328	Sequence 328, App
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1143	190	6.1	1119	2	US-09-904-462-294	Sequence 294, App	1216	182.5	5.8	379	3	US-10-124-822-328	Sequence 328, App
1144	190	6.1	1119	2	US-09-902-736A-294	Sequence 294, App	1217	182.5	5.8	379	3	US-10-223-081-30	Sequence 30, Appl
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1147	190	6.1	1119	2	US-09-903-562B-294	Sequence 294, App	1220	182.5	5.8	379	3	US-10-142-419-328	Sequence 328, App
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1155	190	6.1	1119	3	US-10-147-512-352	Sequence 352, App	1228	182.5	5.8	379	3	US-10-131-822A-328	Sequence 328, App
1156	190	6.1	1119	3	US-09-907-942-294	Sequence 294, App	1229	182.5	5.8	379	3	US-10-142-763-328	Sequence 328, App
1157	190	6.1	1119	3	US-09-906-815C-294	Sequence 294, App	1230	182.5	5.8	379	3	US-10-128-694A-328	Sequence 328, App
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1168	190	6.1	1119	3	US-10-145-873-352	Sequence 352, App	1241	182.5	5.8	966	3	US-10-424-233-22	Sequence 22, Appl
1169	190	6.1	1119	3	US-10-152-395-352	Sequence 352, App	1242	182	5.8	378	2	US-09-689-486-62	Sequence 62, Appl
1170	190	6.1	1119	3	US-10-131-822A-352	Sequence 352, App	1243	182	5.8	378	2	US-09-973-424A-62	Sequence 62, Appl
1171	190	6.1	1119	3	US-10-142-763-352	Sequence 352, App	1244	180	5.7	493	2	US-10-037-417-30	Sequence 30, Appl
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1173	190	6.1	1119	3	US-10-123-213-352	Sequence 352, App	1246	179.5	5.7	308	3	US-10-173-999-68	Sequence 68, Appl
1174	190	6.1	1119	3	US-10-123-909-352	Sequence 352, App	1247	179.5	5.7	515	3	US-10-162-335-92	Sequence 92, Appl
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1178	190	6.1	1119	3	US-10-147-513-352	Sequence 352, App	1251	179	5.7	290	2	US-10-068-426-12	Sequence 12, Appl
1179	190	6.1	1119	3	US-10-121-043-352	Sequence 352, App	1252	179	5.7	290	3	US-10-382-758-10	Sequence 10, Appl
1180	190	6.1	1119	3	US-10-963-467-294	Sequence 294, App	1253	179	5.7	290	3	US-10-382-758-11	Sequence 11, Appl
1181	190	6.1	1119	3	US-10-448-923-294	Sequence 294, App	1254	179	5.7	290	3	US-10-382-758-12	Sequence 12, Appl
1182	190	6.1	1119	3	US-10-139-980-352	Sequence 352, App	1255	179	5.7	302	2	US-10-068-426-8	Sequence 8, Appli
1183	189.5	6.0	301	2	US-10-068-426-9	Sequence 9, Appli	1256	179	5.7	302	3	US-10-382-758-8	Sequence 8, Appli
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1325	178	5.7	1049	3	US-10-013-917A-496	Sequence 496, App	1398	173.5	5.5	421	3	US-10-147-513-302	Sequence 302, App
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1338	178	5.7	1049	3	US-10-124-822-358	Sequence 358, App	1411	172.5	5.5	359	2	US-08-458-834-4	Sequence 4, Appli
1339	178	5.7	1049	3	US-10-165-247A-496	Sequence 496, App	1412	172.5	5.5	359	2	US-09-538-092-868	Sequence 868, App
1340	178	5.7	1049	3	US-10-017-086A-496	Sequence 496, App	1413	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap



QY 241 SHVTLASPESTRCHFPKNAAGRLLELDYADFQCPATTTTATVPTTRPVVREPTALSSSL 300  
Db 241 SHVTLASPESTRCHFPKNAAGRLLELDYADFQCPATTTTATVPTTRPVVREPTALSSSL 300  
QY 301 APTWLSPTATAPSPSPSTAPPTVGPVPOQDCPSTCLNGGTCHLGRHHLACLCEG 360  
Db 301 APTWLSPTATAPSPSPSTAPPTVGPVPOQDCPSTCLNGGTCHLGRHHLACLCEG 360  
QY 361 FTGLYCESQMGQGTTRPSTFTVTPRPRSLTLGIEPVSTSLRVGLQRYLQSSVQLRSLR 420  
Db 361 FTGLYCESQMGQGTTRPSTFTVTPRPRSLTLGIEPVSTSLRVGLQRYLQSSVQLRSLR 420  
QY 421 LTVRNLSGDPKRLVTLRLPASLAEYVTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480  
Db 421 LTVRNLSGDPKRLVTLRLPASLAEYVTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480  
QY 481 PPAVHNSHAPVTOAREGNPLLTAPALAAVLLAALAAVGAAYCVRGRMAAAQDKGV 540  
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QY 541 GPGAGPLELEBVGKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLQSPHLHAKPYI 598  
Db 541 GPGAGPLELEBVGKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLQSPHLHAKPYI 598

RESULT 2

US-09-944-457-69  
; Sequence 69, Application US/09944457  
; Patent No. 6734288  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-944-457-69  
Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MCSRVPLLLPLLLLALGPGVQCGPCGCGSQQTVECTARQGTTPRDPVPPDTVGLYVF 60  
Db 1 MCSRVPLLLPLLLLALGPGVQCGPCGCGSQQTVECTARQGTTPRDPVPPDTVGLYVF 60  
Qy 61 ENGITMLDASSFAGLPGLQLLDLSQNIASRLPRLLLLDLSHNSLLALEPGLDITANVE 120  
Db 61 ENGITMLDASSFAGLPGLQLLDLSQNIASRLPRLLLLDLSHNSLLALEPGLDITANVE 120

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QY 121 ALRLAGLGLQOQDEGLFSRLRNHLVDSDNQLERVPVIRGLRGLTRLELAGNTRIAQL 180
Db 121 ALRLAGLGLQOQDEGLFSRLRNHLVDSDNQLERVPVIRGLRGLTRLELAGNTRIAQL 180
QY 181 RPEDLAGLAALQELQDLSNLSQALPGDLGSLFPRLLRLLAAARNPFCVPLSFGFPWVRE 240
Db 181 RPEDLAGLAALQELQDLSNLSQALPGDLGSLFPRLLRLLAAARNPFCVPLSFGFPWVRE 240
QY 241 SHVTLASPETRCHFPFKPKNAGRLLELDYADFQCPATTTATVTPTRPVVREPTALSSSL 300
Db 241 SHVTLASPETRCHFPFKPKNAGRLLELDYADFQCPATTTATVTPTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEARSPPTAPPTVCPVPQDQCPSTCLNGCTCHLGRHHLACLCPEG 360
Db 301 APTWLSPTAPATEARSPPTAPPTVCPVPQDQCPSTCLNGCTCHLGRHHLACLCPEG 360
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Db 361 FTGLYCESQMGOTRPSPTVTPRPRSLTLGTPEVSPTSRLVGLORYLOGSSVQLRSRLR 420
QY 421 LTYRNLGSGDKRLVTLRLPASLAETVTTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
Db 421 LTYRNLGSGDKRLVTLRLPASLAETVTTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
QY 481 PPAVSHNAPVTOAREGNPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAADKQGV 540
Db 481 PPAVSHNAPVTOAREGNPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAADKQGV 540
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGEALPGSSECEVPLMGPPGLOSLPHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGEALPGSSECEVPLMGPPGLOSLPHAKPYI 598

RESULT 3
US-09-945-584-69
; Sequence 69, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
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Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGFGVGCPCGQCQSQBOTVCTARQGTTPRDPVPPDTVGLYVF 60  
DB 1 MCSRVPLLLPLLLLLALGFGVGCPCGQCQSQBOTVCTARQGTTPRDPVPPDTVGLYVF 60  
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DB 61 ENGITMLDASSFAGLPGQLQLDLDSQNCIASRLPRLLLLDLSDNSLLALEPGLDNTANVE 120  
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DB 121 ALRLAGLGLQQLDEGLFSRLNLHDLSDNQLRVPVPIRGLRGLTRLAGNTRIAQL 180  
QY 181 RPEDLAGLAAQLBELDVSNLSLOALPGDLGSLFPRLLRLAAARNPFCVPLSFGPWVRE 240  
DB 181 RPEDLAGLAAQLBELDVSNLSLOALPGDLGSLFPRLLRLAAARNPFCVPLSFGPWVRE 240  
QY 241 SHVTLASPEETRCHFPKNGRLLLELDVADFCGCPATTTTATVPTTRPVVREPTALSSSL 300  
DB 241 SHVTLASPEETRCHFPKNGRLLLELDVADFCGCPATTTTATVPTTRPVVREPTALSSSL 300  
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DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPATYSVCVMPGLPGRVPGEERACGAHT 480  
QY 481 PPAVHNHAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVRRGRMAAAADKGOV 540  
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DB 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598

## RESULT 4

US-09-944-944-69  
; Sequence 69, Application US/09944944  
; Patent No. 6929947  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944, 944  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866, 028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067, 411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 425  
; PRIOR FILING DATE: December 12, 1997  
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; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 694  
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; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068, 017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070, 440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074, 086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074, 092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075, 945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112, 850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113, 296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146, 222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216, 021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218, 517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254, 311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6929947ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6929947ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-944-69

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.2e-216;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLALGFGVQCPCGSCQSQQTVFCTARQGTTPVDRVPPDVTGLYVF 60
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QY 61 ENGITWLDASSFAGLPGIQLDLSNQIASRLPRLLLDLSNSLLALEPGLDITANVE 120
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QY 121 ALRLAGLGIQQLDDEGLFSRLNHLHDVSDNQLERVPPVIRGLRGLTRLEAGNTRIAQL 180
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QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRRLRLAAARNPFNCVPLSFGFPWVRE 240
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QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFQCPATTTTATVPTTRPVVREPTALSSSL 300
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QY 301 APTWLSPTAPATEAPSPSTAPTVCVPQPOQDCPSTCLNGTCHLGRHHLACI CPEG 360
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QY 361 FTGLYCESOMGCGTRPSPTVTPRPRPSRLTLGIEPVSPTSRLVGLORYLQSSVQLRSRLR 420
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QY 421 LTYRNLSPDKRLVTLRLPASLAETVTTQLRPNATYSVCVMPLGPRVPEGEACGEAHT 480
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QY 481 PPAVSHNHAPVTQAREGNLPILLIAPALAAVLAALAAVGAAYCVRGRGMAAAQDKGV 540
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RESULT 5
; Sequence 69, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PIC1

; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
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; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-945-587-69

Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MCSRVPLLLPLLLALLGPGVQCPCGCGCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60  
  
QY 61 ENGITWLDASSFAGLPGQLQLDLSONQIASRLPRLLLDLSHNSLLALEPGILDITANVE 120  
DB 61 ENGITWLDASSFAGLPGQLQLDLSONQIASRLPRLLLDLSHNSLLALEPGILDITANVE 120  
  
QY 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDVNDQNLERVPVIRGLRGLTRLAGNTRIAQL 180  
DB 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDVNDQNLERVPVIRGLRGLTRLAGNTRIAQL 180  
  
QY 181 RPEDLAGLALQELDVSNLSLOALPGDLGSLFPRLRLAARPNFNCVPLSFWGPPVRE 240  
DB 181 RPEDLAGLALQELDVSNLSLOALPGDLGSLFPRLRLAARPNFNCVPLSFWGPPVRE 240  
  
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300  
DB 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300  
  
QY 301 APTWLSPTAPATEAPSPPTAPPTVGPVPOQPCPSTCLNGGTCCHLGRHHLACLCPGEG 360  
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DB 361 FTGLYCESQMGQGTTRSPPTVTPRPRSLTLGIEPVSPVSLRVGLQRYLOGSSVOLRSRLR 420  
  
QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTLRPNATYSVCVMPGLGPGRVPEGEACGEAHT 480  
DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTLRPNATYSVCVMPGLGPGRVPEGEACGEAHT 480  
  
QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKQGV 540  
DB 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKQGV 540  
  
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DB 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598

RESULT 6

US-09-944-884-69  
; Sequence 69, Application US/09944884  
; Patent No. 7018837  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-944-884-69

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLALLGPGVQCPCGCGCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60  
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DB 61 ENGITWLDASSFAGLPGQLQLDLSONQIASRLPRLLLDLSHNSLLALEPGILDITANVE 120  
  
QY 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDVNDQNLERVPVIRGLRGLTRLAGNTRIAQL 180  
DB 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDVNDQNLERVPVIRGLRGLTRLAGNTRIAQL 180  
  
QY 181 RPEDLAGLALQELDVSNLSLOALPGDLGSLFPRLRLAARPNFNCVPLSFWGPPVRE 240  
DB 181 RPEDLAGLALQELDVSNLSLOALPGDLGSLFPRLRLAARPNFNCVPLSFWGPPVRE 240  
  
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300  
DB 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300  
  
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DB 301 APTWLSPTAPATEAPSPPTAPPTVGPVPOQPCPSTCLNGGTCCHLGRHHLACLCPGEG 360  
  
QY 361 FTGLYCESQMGQGTTRSPPTVTPRPRSLTLGIEPVSPVSLRVGLQRYLOGSSVOLRSRLR 420  
DB 361 FTGLYCESQMGQGTTRSPPTVTPRPRSLTLGIEPVSPVSLRVGLQRYLOGSSVOLRSRLR 420  
  
QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTLRPNATYSVCVMPGLGPGRVPEGEACGEAHT 480  
DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTLRPNATYSVCVMPGLGPGRVPEGEACGEAHT 480  
  
QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKQGV 540  
DB 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKQGV 540  
  
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598  
DB 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598

RESULT 7

US-10-219-074-104  
; Sequence 104, Application US/10219074  
; Patent No. 7129324  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey



```

: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530PIC70
: CURRENT APPLICATION NUMBER: US/10/219,074
: CURRENT FILING DATE: 2002-08-13
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 104
: LENGTH: 598
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-219-074-104

Query Match          100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.2e-216;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1  MCSRVPELLLLLLALGPGVGCGSGCQSQPQTVCFTARQTTVPRDVPDPTVGLYVF 60
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Qy      121  ALRIAGLGLQQLDEGLFRLRLNHLVDSDNOLERVPPVIRGLGILTRILRLAGNTRIAQL 180
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Qy      181  RPEDLAGLAALQEDVDVSNLSLQALPGDLSGLFPRLRLAAARNPNCVCLSWFGPWVRE 240
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Qy      241  SHVTLASPEETRCHFPFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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Qy      301  APTWLSPTAPATEAPSPSTAPPTVGPVPQDQCPSTCLNGGTCHLGTRHHLACLCPBG 360
Db      301  APTWLSPTAPATEAPSPSTAPPTVGPVPQDQCPSTCLNGGTCHLGTRHHLACLCPBG 360

Qy      361  FTGLYCSQMOGGTPEPTVTPRPRSILGIEPVSPSLRVLGVQRYLQGSVOLRSRLR 420
Db      361  FTGLYCSQMOGGTPEPTVTPRPRSILGIEPVSPSLRVLGVQRYLQGSVOLRSRLR 420

Qy      421  LTYRNLSGDPKRLVTRLPASLAETVTLQLRPNATYVSCVMPGLGRCRVPGEAGEAHT 480

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Db	421	LTYRNLSGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPLGPRVPEGEACGEAHT	480
Qy	481	PPAVSHNHAPVTQAREGNLPLLIIAPALAAVLLAALAAVGAAYCVRRRGRAMAAAOQKGOV	540
Db	481	PPAVSHNHAPVTQAREGNLPLLIIAPALAAVLLAALAAVGAAYCVRRRGRAMAAAOQKGOV	540
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Db	541	GPAGAPLELEGVKVPLPGPKATGGGSECEVPLMGFPQGLQSPHAKPYI	598
RESULT 8			
US-10-227-873-104			
; Sequence 104, Application US/10227873			
; Patent No. 7129325			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Geritsen, Mary			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stephan, Jean-Philippe F.			
; APPLICANT: Watanabe, Colin L.			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: F3530P1C72			
; CURRENT APPLICATION NUMBER: US/10/227,873			
; CURRENT FILING DATE: 2002-08-26			
; PRIOR APPLICATION NUMBER: 10/119,480			
; PRIOR FILING DATE: 2002-04-09			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
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; PRIOR APPLICATION NUMBER: 60/089532			
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; PRIOR APPLICATION NUMBER: 60/089905			
; PRIOR FILING DATE: 1998-06-18			



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; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-11-18  
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; PRIOR FILING DATE: 1999-07-28  
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; PRIOR FILING DATE: 1999-12-07  
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; PRIOR FILING DATE: 1999-12-07  
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MCSRVPLLLPLLLLLALGPGVQCSCQCSQPTVCTARQGTTPRDPVPPDTVGLYVF 60  
QY 61 ENGITWLDASSFAGLPGQLLDLSQNOIASRLPRLLLDLSHNSLLALEPGLDITANVE 120  
Db 61 ENGITWLDASSFAGLPGQLLDLSQNOIASRLPRLLLDLSHNSLLALEPGLDITANVE 120  
QY 121 ALRLAGLGLQQLDEGLFSRLNLDLSDNQLERVPVIRGLRGLTRLAGNTRIAQL 180  
Db 121 ALRLAGLGLQQLDEGLFSRLNLDLSDNQLERVPVIRGLRGLTRLAGNTRIAQL 180  
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFPRRLRLAAARNPFCVCLSWFGPWVRE 240  
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Db 481 PPAVHNSHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAADKQGV 540  
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RESULT 9

US-10-218-849-104  
; Sequence 104, Application US/10218849  
; Patent No. 7144990  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C11  
; CURRENT APPLICATION NUMBER: US/10/218,849  
; PRIOR FILING DATE: 2002-08-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 104  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-218-849-104

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MCSRVPLLLPLLLLLALGPGVQCSCQCSQPTVCTARQGTTPRDPVPPDTVGLYVF 60  
QY 61 ENGITWLDASSFAGLPGQLLDLSQNOIASRLPRLLLDLSHNSLLALEPGLDITANVE 120  
Db 61 ENGITWLDASSFAGLPGQLLDLSQNOIASRLPRLLLDLSHNSLLALEPGLDITANVE 120  
QY 121 ALRLAGLGLQQLDEGLFSRLNLDLSDNQLERVPVIRGLRGLTRLAGNTRIAQL 180  
Db 121 ALRLAGLGLQQLDEGLFSRLNLDLSDNQLERVPVIRGLRGLTRLAGNTRIAQL 180  
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFPRRLRLAAARNPFCVCLSWFGPWVRE 240  
Db 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFPRRLRLAAARNPFCVCLSWFGPWVRE 240  
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFCGPAITTTTATVPTTRPVVREPTALSSSL 300  
Db 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFCGPAITTTTATVPTTRPVVREPTALSSSL 300  
QY 301 APTWLSPTAPATEAPSPPTAPPTVGPVQPCPPSTCLNGGTCCHLGRHHLACLCEG 360  
Db 301 APTWLSPTAPATEAPSPPTAPPTVGPVQPCPPSTCLNGGTCCHLGRHHLACLCEG 360  
QY 361 FTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVQLRSRLR 420  
Db 361 FTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVQLRSRLR 420  
QY 421 LTYRNLGPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLGPRVPEGEACGEAHT 480  
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Db 541 GPGAGFLEGVKVPLEPGKATEGGGEALPGSSECEVPLMGPPGLQSPHAKPYI 598

RESULT 10

US-10-216-168-104  
; Sequence 104, Application US/10216168  
; Patent No. 7157558  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C10  
; CURRENT APPLICATION NUMBER: US/10/216,168  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31

100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-216;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 MCSRVPLILPLILLLALGVCQCPGCGCCQSQPQVFTCTARQGTTPRDVPPDTVGLYVF 60  
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181 RPEDLAGLAAQLDLSVNSLSQALPGDLSGLFPRRLRLAAARNPFCVPLSFWGPVWRE 240  
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481 PPAVHSHNAPVTOAREGNLPLLLIAPALAAVLLAALAAVGAAYCVRGRMAAAQAQDKGV 540  
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541 GPGAGPLEGKVPLEPGPKATEGGGEALPSGSECEVPLMGPGPLQSPHAKPYI 598

RESULT 11

US-09-944-896-69  
Sequence 69, Application US/09944896  
Patent No. 7189566  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Botstein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Kljavin, Ivar  
APPLICANT: Napier, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tamas, Daniel  
APPLICANT: Wood, William  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P2548P1C1  
CURRENT APPLICATION NUMBER: US/09/944, 896  
CURRENT FILING DATE: 2001-08-31  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 09/866, 028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/069, 334  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069, 335  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069, 278  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069, 425  
PRIOR FILING DATE: December 12, 1997  
PRIOR APPLICATION NUMBER: 60/069, 696  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069, 694  
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PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/069, 873  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/068, 017  
PRIOR FILING DATE: December 18, 1997  
PRIOR APPLICATION NUMBER: 60/070, 440  
PRIOR FILING DATE: January 5, 1998  
PRIOR APPLICATION NUMBER: 60/074, 086  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/074, 092  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/075, 945  
PRIOR FILING DATE: February 25, 1998  
PRIOR APPLICATION NUMBER: 60/112, 850  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 60/113, 296  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 60/146, 222  
PRIOR FILING DATE: July 28, 1999  
PRIOR APPLICATION NUMBER: PCT/US98/19330  
PRIOR FILING DATE: September 16, 1998  
PRIOR APPLICATION NUMBER: PCT/US98/25108  
PRIOR FILING DATE: December 1, 1998  
PRIOR APPLICATION NUMBER: 09/216, 021  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 09/218, 517  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 09/254, 311  
PRIOR FILING DATE: March 3, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: June 22, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: September 15, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28409  
PRIOR FILING DATE: No. 7189566ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: No. 7189566ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28301  
PRIOR FILING DATE: December 1, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/30095

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; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO: 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-896-69

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Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.2e-216;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085

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; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-063-950-2

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Query Match      98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 6.7e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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DB 421 LTRYRLSGPDKRLVTLRLPASIAEYTVQLRPNATYSCVMPPLGPRVVEGEACGEAHT 480
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RESULT 13
US-09-991-181-52
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:

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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PJC53  
CURRENT APPLICATION NUMBER: US/09/991,181  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1997-11-24  
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PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;  
Best Local Similarity 88.7%; Pred. No. 6,7e-213;  
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRRPLLLPLLLALLGSGVGGCCGCCSQPQVFCFARQCTTVPRDVPPTVGLYVF 60  
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DB 61 ENGIMLDASFPAGLPGQLDLDSQNOIASLPSGCVFQPLANLSNDLTLNRLHETNEFF 120  
QY 91 -----LRLPRLLLDLSHNS 105  
DB 121 RGLRLRLRYLGNRIIRHIOGAFPTLDRLELKLQDNELRALPLRLPLRLLLDLSHNS 180  
QY 106 LLALEPGILDPTANVEALRLAGLGLQQLDEGLFSRLNHLDDVSDNQLERVVPVINGLKG 165  
DB 181 LLALEPGILDPTANVEALRLAGLGLQQLDEGLFSRLNHLDDVSDNQLERVVPVINGLKG 240  
QY 166 LTRLRLAGNTRIAQLRPEDLAGLALQELDVSNLSIQALPGDLSGLFPRRLTLAAARNPF 225

DB 241 LTRLRLAGNTRIAQLRPEDLAGLALQELDVSNLSIQALPGDLSGLFPRRLTLAAARNPF 300  
QY 226 NCVCPLSMFGPWWRESHTVLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPT 285  
DB 301 NCVCPLSMFGPWWRESHTVLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPT 360  
QY 286 TRPVREPTALSSSLAPTWLSPTAPATAPSPSTAPPTVGPVPODDCPSTCLNGCTC 345  
DB 361 TRPVREPTALSSSLAPTWLSPTAPATAPSPSTAPPTVGPVPODDCPSTCLNGCTC 420  
QY 346 HLGTRHHLACLCEPGFGYLCESOMGGCTRBSPPVPTPRPRSLLTGIEPVSPSLRGL 405  
DB 421 HLGTRHHLACLCEPGFGYLCESOMGGCTRBSPPVPTPRPRSLLTGIEPVSPSLRGL 480  
QY 406 QRYLOGSSVOLRSRLTYRNLGSPDKLVTLRLPASLAEYVTOLRPNATYSCVMPGCP 465  
DB 481 QRYLOGSSVOLRSRLTYRNLGSPDKLVTLRLPASLAEYVTOLRPNATYSCVMPGCP 540  
QY 466 GRVPEGEACGEAHTPPAVSHNAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525  
DB 541 GRVPEGEACGEAHTPPAVSHNAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600  
QY 526 RGRMAAAADQKQVGGAPLELEGYKVLBRPKATBEGGELPBGSGEVEVPLMGFP 585  
DB 601 RGRMAAAADQKQVGGAPLELEGYKVLBRPKATBEGGELPBGSGEVEVPLMGFP 660  
QY 586 PGLQSPPLHAKPYI 598  
DB 661 PGLQSPPLHAKPYI 673

RESULT 14  
US-09-990-444-52  
Sequence 52, Application US/09990444  
Patent No. 6930170  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavrin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C19  
CURRENT APPLICATION NUMBER: US/09/990,444  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311



PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;  
Best Local Similarity 88.7%; Pred. No. 6.7e-213;  
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLPLLLALAGVGCSPGSCCQSPQVFTCTAROGTTVPDPVPTVGLVYF 60  
DB 1 MCSRVPLLLPLLLALAGVGCSPGSCCQSPQVFTCTAROGTTVPDPVPTVGLVYF 60  
QY 61 ENGITMLDASSFAGLPGIQLDLISQNOIAS----- 90  
DB 61 ENGITMLDASSFAGLPGIQLDLISQNOIAS----- 90  
QY 91 -----LRPLLLLDLSHNS 105  
DB 121 RGLRRLERLYGKNRI RHIOGAPDITDLRLLEKIDNELRALPLRLPLLLLDLSHNS 180  
QY 106 LLALPGLIDTANVALRLAGLGLDGLFSRLNLDLVDSDNQLERVPVIRGLNG 165  
DB 181 LLALPGLIDTANVALRLAGLGLDGLFSRLNLDLVDSDNQLERVPVIRGLNG 240  
QY 166 LTRRLAGNTRIAQLRPEDLAGLALQELDVNSLQALPGDISGLFPRLRLAAARNPF 225  
DB 241 LTRRLAGNTRIAQLRPEDLAGLALQELDVNSLQALPGDISGLFPRLRLAAARNPF 300  
QY 226 NCVCPLSNFGPWVRSHTVLASPEETRCFPKPNAGRLLELDYADFGCPATTTATVPT 285  
DB 301 NCVCPLSNFGPWVRSHTVLASPEETRCFPKPNAGRLLELDYADFGCPATTTATVPT 360  
QY 286 TRPVVREPTALSSSLAPTMLSPTATPTEAPSPSTAPTVGPVPODCEPSTCLNGGTC 345  
DB 361 TRPVVREPTALSSSLAPTMLSPTATPTEAPSPSTAPTVGPVPODCEPSTCLNGGTC 420  
QY 346 HLGTRHNLACLPESFTGLYCESQMGQGRPSPTVTPRPPRSLLTGIEPVSTSLRVGL 405  
DB 421 HLGTRHNLACLPESFTGLYCESQMGQGRPSPTVTPRPPRSLLTGIEPVSTSLRVGL 480  
QY 406 QRYLOGSSVQLRSLRTYRNLSGPDRLVTLRLPASLAEYTVTQLRPNAATYSCVMPDGP 465  
DB 481 QRYLOGSSVQLRSLRTYRNLSGPDRLVTLRLPASLAEYTVTQLRPNAATYSCVMPDGP 540  
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DB 541 GRVPEGEACGAEHTPPAVHSNHAPVTOAREBNLPLILPALAAVLLAALAAVGAAYCTR 600  
QY 526 RGRMAAAADODKGVGPGAGPLEEGVKVLEPGPKATEGGEBALPSGSECEVPLMGFPFG 585  
DB 601 RGRMAAAADODKGVGPGAGPLEEGVKVLEPGPKATEGGEBALPSGSECEVPLMGFPFG 660  
QY 586 PGLQSPHLAKPYI 598  
DB 661 PGLQSPHLAKPYI 673

RESULT 15  
US-09-997-333-52  
; Sequence 52, Application US/09997333  
; Patent No. 6953836

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumaas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
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PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
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PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326





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Db 301 NCVCPLSWFGPWVRSHTYLAASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPT 360
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Db 601 RGRMAAAAADKQGVGPGAGPLELGGVKVPLEPGPKATEGGGBALPSGSBCEVPLMGFPG 660
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QY 586 PGLQSPILHAKPYI 598
    |||||||
Db 661 PGLQSPILHAKPYI 673
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Search completed: August 29, 2007, 08:48:29  
Job time : 95 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: August 29, 2007, 08:46:46 ; Search time 43 Seconds  
(without alignments)  
1338.084 Million cell updates/sec

Title: US-09-943-780-69

Perfect score: 3135  
Sequence: 1 MCSRVPLLLPLLLALGPG.....PLMGPPGGLQSLHAKPYI 598

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322	10.3	605	2	JCS239
2	302	9.6	605	2	A41915
3	282	9.0	626	1	NBHUIA
4	281.5	9.0	603	2	JC1282
5	278.5	8.9	603	2	JC6128
6	278	8.9	1531	2	T42218
7	264.5	8.4	420	2	A53531
8	261	8.3	1523	2	T13953
9	255.5	8.1	1469	2	B36655
10	255.5	8.1	1480	2	A36655
11	251	8.0	622	1	JC7973
12	243.5	7.8	312	1	NBHUA2
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14	237	7.6	707	2	JC7763
15	231	7.4	1025	2	T42626
16	222.5	7.1	536	2	A34901
17	214.5	6.8	1535	2	A46224
18	212.5	6.8	361	2	A53860
19	210.5	6.7	4302	2	A38971
20	209	6.7	1091	2	A58532
21	208.5	6.7	653	2	T25194
22	200	6.4	653	2	T23007
23	199	6.3	1328	2	T28714
24	194.5	6.2	789	2	T28715
25	194.5	6.2	1355	2	T28715
26	193.5	6.2	421	2	T46266
27	193.5	6.2	721	2	E70766
28	192.5	6.1	575	2	T29972
29	189	6.0	369	2	S20811

30	189	6.0	369	2	S32793	biglycan precursor
31	189	6.0	839	2	T04859	extensin homolog F
32	188.5	6.0	440	2	A47530	oligodendrocyte-my
33	186	5.9	440	2	A39613	oligodendrocyte-my
34	184	5.9	368	1	BGHUN	biglycan precursor
35	183	5.8	662	2	S42799	garp precursor - h
36	182	5.8	369	2	S32559	biglycan precursor
37	181.5	5.8	357	2	S24317	decorin precursor
38	177.5	5.7	2493	2	A55481	adenylate cyclase
39	176.5	5.6	1495	2	T31434	densin-180 - rat
40	175	5.6	343	2	A41748	lumican precursor
41	173	5.5	925	2	JC2033	G protein-coupled
42	172.5	5.5	359	1	NBHUC8	decorin precursor
43	172	5.5	1134	2	T04587	hypothetical prote
44	170.5	5.4	2145	2	JC4747	adenylate cyclase
45	170	5.4	907	2	JE0176	orphan G protein-c
46	169.5	5.4	760	2	T06291	extensin homolog T
47	169	5.4	354	2	A54548	decorin precursor
48	169	5.4	839	2	F75518	hypothetical prote
49	168.5	5.4	907	2	JG0193	G protein-coupled
50	167	5.3	800	2	S37387	intermalin A precu
51	167	5.3	1112	2	T10504	disease resistance
52	166.5	5.3	549	2	T41744	hypothetical prote
53	166.5	5.3	800	2	AB1129	internalin A limpo
54	165.5	5.3	360	2	S06280	decorin precursor
55	165.5	5.3	526	2	C84552	hypothetical prote
56	165.5	5.3	1256	2	S60461	gene flightless-I
57	165.5	5.3	1268	2	A49674	flightless-I homol
58	165	5.3	994	2	H96510	probable disease r
59	163.5	5.2	786	2	T01456	extensin homolog F
60	162	5.2	242	2	T14791	hypothetical prote
61	161	5.1	559	2	T42998	Ras-binding protei
62	161	5.1	682	2	A49121	cell-surface molec
63	161	5.1	682	2	A43118	connectin precurs
64	160.5	5.1	2910	2	T42214	otogelin - mouse
65	160	5.1	744	2	B86255	hypothetical prote
66	159.5	5.1	1112	2	T00952	hypothetical prote
67	159	5.1	572	2	T30947	protein AC7.2 (imp
68	159	5.1	613	2	A86884	hypothetical prote
69	159	5.1	702	2	T21148	hypothetical prote
70	158.5	5.1	1119	2	AD1822	leucine-rich-repea
71	158.5	5.1	738	2	T13938	hypothetical prote
72	158	5.0	1066	2	T15864	hypothetical prote
73	158	5.0	3570	2	T45025	mucin MUC5B, trach
74	156.5	5.0	360	2	I47020	decorin - rabbit
75	156.5	5.0	980	2	H84632	probable receptor-
76	156	5.0	354	2	S29145	decorin precursor
77	156	5.0	993	2	T23841	hypothetical prote
78	155.5	5.0	903	2	T00705	N-chimerin homolo
79	155.5	5.0	1334	2	T23395	probable multi-dom
80	155	4.9	961	2	T23395	hypothetical prote
81	154.5	4.9	1013	2	T10659	probable serine/th
82	154.5	4.9	1143	2	T10636	hypothetical prote
83	154.5	4.9	1192	2	T48499	receptor-like prot
84	154.5	4.9	1495	2	S60255	transcription co-r
85	153.5	4.9	864	2	T08575	protein kinase hom
86	153.5	4.9	894	1	A41527	protein-tyrosine k
87	153	4.9	699	2	C43574	US4 protein - huma
88	152	4.8	786	2	T08664	Toll protein-like
89	151.5	4.8	695	1	JN0898	folliculotropin recept
90	151	4.8	540	2	T12704	leucine-rich prote
91	151	4.8	1389	2	T13852	gene wheeler prote
92	151	4.8	685	1	ORHUF2	folliculotropin recept
93	150.5	4.8	1109	2	T18536	receptor-like prot
94	150	4.8	1134	1	A29944	chaoptin precursor
95	149.5	4.8	224	2	T32185	hypothetical prote
96	149.5	4.8	696	1	JC7361	folliculotropin recept
97	149	4.8	1025	1	A57676	protein kinase Xa2
98	149	4.8	1143	2	B84431	probable receptor
99	149	4.8	2357	2	A59249	class VII unconven
100	148.5	4.7	375	2	S05390	fibromodulin precu
101	148.5	4.7	610	2	T23836	hypothetical prote
102	148.5	4.7	680	2	T19939	hypothetical prote

103	148.5	4.7	890	2	C96654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	JC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	D83333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	ALR protein - huma
108	147.5	4.7	316	2	A41781	proteoglycan-Lb -	181	135	4.3	601	2	S56144	SH3 domain binding
109	147.5	4.7	1385	2	T13887	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T09059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hyLB homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	G83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S18706	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S29605	glycoprotein 350/2	190	133.5	4.3	1068	2	H96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	MHC class III hist	191	133	4.2	576	2	T36729	probable serine/th
119	145	4.6	458	2	T15941	hypothetical prote	192	133	4.2	852	2	I51259	tyrosine kinase C
120	145	4.6	679	2	T20713	hypothetical prote	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2237	hypothetical prote	194	133	4.2	1257	2	A88536	protein B0523.5 [1
122	145	4.6	1839	1	OVBVK	follitropin recept	195	133	4.2	4391	2	A85096	perlecan precursor
123	144.5	4.6	486	2	B86460	adenylate cyclase	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T30826	nascent polypeptid	197	132.5	4.2	2035	2	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0BE8	Bpfr1 protein - hu	198	132	4.2	3164	1	WMBH6	UL36 protein - hum
126	144	4.6	695	2	I45896	follicle stimulati	199	131.5	4.2	346	2	T46916	hypothetical prote
127	144	4.6	1019	2	C96519	probable disease r	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	mucin 2 precursor,	201	131.5	4.2	1097	2	A29943	Toll protein precu
129	143.5	4.6	243	2	B41710	hypothetical prote	202	131.5	4.2	1286	2	A88396	protein kinase Xa2
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	612	2	T10727	probable LRR recep
131	143.5	4.6	496	2	C96832	hypothetical prote	204	131	4.2	767	2	B84594	probable disease r
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	905	2	T00475	smoothelin - human
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	915	2	T09575	hypothetical prote
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1095	2	G96746	brassinosteroid-in-
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	1196	2	T09356	hypothetical prote
136	142	4.5	661	2	I56258	RPI05 - mouse	209	130.5	4.2	448	2	T27395	hypothetical prote
137	142	4.5	983	2	D84524	probable disease r	210	130	4.1	268	2	T19697	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	389	2	H86266	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	395	2	H75457	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	768	2	T17462	disease resistance
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	800	2	H84740	hypothetical prote
142	141	4.5	630	2	AC1129	internalin B [impo	215	129.5	4.1	315	2	T06806	proline rich prote
143	141	4.5	717	2	T33295	hypothetical prote	216	129.5	4.1	780	2	T00366	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu	217	129.5	4.1	861	2	A48825	Notch homolog Motc
145	140	4.5	277	2	I60122	rsu-1 homolog - hu	218	129.5	4.1	912	2	A54423	brevican precursor
146	140	4.5	474	2	S65763	chitinase [SC 3.2	219	129.5	4.1	942	2	S23251	protein-tyrosine k
147	140	4.5	754	2	A85043	probable LRR recep	220	129.5	4.1	1173	2	I50620	prockr2 - chicken
148	140	4.5	1029	2	T00712	protein kinase hom	221	129.5	4.1	1459	2	T09219	basal transcriptio
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	371	2	S20075	promastigote surfa
150	139.5	4.4	527	2	A75399	hypothetical prote	223	129	4.1	930	2	T05259	probable disease r
151	139.5	4.4	539	2	G70520	probable csp prote	224	129	4.1	815	2	B96770	hypothetical prote
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra	225	129	4.1	1027	2	B85089	receptor protein k
153	139	4.4	581	2	A45551	insect-stage-speci	226	129	4.1	1064	2	B86465	probable Protein k
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1232	2	T05322	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1329	2	A64828	cell division prot
156	139	4.4	1088	2	E86312	FlilA6.9 protein -	229	129	4.1	1342	2	B85614	cell division prot
157	139	4.4	2240	2	T37057	probable multi-dom	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	lumican precursor	231	129	4.1	1959	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	hypothetical prote	232	129	4.1	2321	2	S78549	notch3 protein - h
160	138.5	4.4	1650	2	S53457	dominant autoantig	233	128.5	4.1	487	2	S42442	nuclear protein EB
161	138	4.4	630	2	C39930	hypothetical prote	234	128.5	4.1	677	2	H86208	protein F265.26 [
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C84534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C84527	probable receptor-
164	137.5	4.4	1151	2	T18535	high molecular mas	237	128.5	4.1	825	2	T29634	hypothetical prote
165	137.5	4.4	4660	2	T42737	gp30 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A44265	trithorax homolog
167	137	4.4	695	2	JC1493	follitropin recept	240	128	4.1	597	2	S72468	probable transcript
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q0BE21	membrane antigen g	242	128	4.1	1428	2	T08852	lustrin A - Califo
170	137	4.4	4544	1	S02392	alpha-2-macroglobu	243	128	4.1	1914	2	T42635	tenascin Y precurs
171	137	4.4	4545	1	S25111	alpha-2-macroglobu	244	127.5	4.1	750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72271	proteoglycan Lb pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	AE0123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	follitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	probable receptor-	248	127	4.1	773	2	T00502	probable receptor-

249	127	4.1	775	1	EDB811	immediate-early pr	322	121.5	3.9	432	2	E86712	unknown protein,
250	127	4.1	800	2	G84740	hypothetical prote	323	121.5	3.9	519	2	T07026	ethylene receptor
251	127	4.1	1366	2	T355985	probable large pro	324	121.5	3.9	635	2	T07794	ethylene receptor
252	127	4.1	1895	2	T06609	disease resistance	325	121.5	3.9	686	2	Tc7569	Delta-4 protein -
253	127	4.1	1955	1	AGCH	agrin precursor -	326	121.5	3.9	760	2	J68387	probable Pto kinase
254	126.5	4.0	685	2	T45516	hypothetical prote	327	121.5	3.9	902	2	T00588	hypothetical prote
255	126.5	4.0	268	2	UC7570	Delta-4 protein -	328	121.5	3.9	1251	2	A57293	hypothetical prote
256	126.5	4.0	694	2	UC4301	foolitoropin recept	329	121.5	3.9	1409	2	T37188	latent transferlin
257	126.5	4.0	862	2	T46289	hypothetical prote	330	121.5	3.9	2265	1	FN80	presynaptic activat
258	126.5	4.0	999	1	S22756	receptor-like prot	331	121.5	3.9	2297	2	T34918	polyketide synthas
259	126.5	4.0	1091	2	T33596	protein-tyrosine k	332	121.5	3.9	2318	2	S45306	notch 3 protein -
260	126.5	4.0	1777	2	T34369	hypothetical prote	333	121.5	3.9	3530	2	A59266	nonconventional myo
261	126	4.0	500	2	S49302	AM01218 protein -	334	121	3.9	306	2	T52340	cell wall-plasma m
262	126	4.0	865	2	A47282	calcium-binding pr	335	121	3.9	480	2	T00971	probable disease r
263	126	4.0	873	2	A47283	calphotin - fruit	336	121	3.9	485	2	A33647	sulfated surface g
264	126	4.0	996	2	F86410	protein F3M18.12 l	337	121	3.9	733	2	A45301	microtubule-associ
265	126	4.0	1152	2	T31911	hypothetical prote	338	121	3.9	1203	2	A49175	Morch B protein -
266	126	4.0	1820	2	A55494	latent transformin	339	121	3.9	1520	2	T00273	hypothetical prote
267	125.5	4.0	283	2	S13383	hydroxyproline-ric	340	121	3.9	2531	2	S18188	notch protein homo
268	125.5	4.0	548	2	AH1107	internalin H limpo	341	120.5	3.8	299	2	A35272	osteolnductive fac
269	125.5	4.0	635	2	F75477	hypothetical prote	342	120.5	3.8	753	2	J00532	OP protein - Kenna
270	125.5	4.0	764	2	A40077	chytrotropin recept	343	120.5	3.8	821	2	AB1126	internalin, peptid
271	125.5	4.0	1003	2	T05898	hypothetical prote	344	120.5	3.8	855	2	T17460	disease resistance
272	125	4.0	350	2	S22456	hydroxyproline-ric	345	120.5	3.8	976	2	B84650	probable receptor-
273	125	4.0	476	2	A36478	surface glycoprote	346	120.5	3.8	976	2	T05897	protein kinase hom
274	125	4.0	783	2	T45899	receptor protein k	347	120.5	3.8	981	2	T50851	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote	348	120.5	3.8	987	2	T50850	receptor protein k
276	125	4.0	991	2	T52400	receptor-like prot	349	120.5	3.8	1118	2	A48292	mucin, tracheobrom
277	125	4.0	1504	2	T49896	glycine/proline-ri	350	120.5	3.8	1152	2	A33183	microtubule-associ
278	125	4.0	2026	1	OYBY	adenylate cyclase	351	120.5	3.8	1722	2	B89753	protein P11C7.4 li
279	124.5	4.0	298	2	B35272	osteolnductive fac	352	120.5	3.8	1778	2	AF1116	internalin protein
280	124.5	4.0	756	2	T27642	hypothetical prote	353	120.5	3.8	3566	1	AA0701	tenascin-X precurs
281	124.5	4.0	849	2	C97303	hypothetical prote	354	120.5	3.8	3761	2	AH1469	internalin protein
282	124.5	4.0	910	2	G84648	probable disease r	355	120	3.8	376	2	S71558	probable cell wall
283	124.5	4.0	977	2	C96745	hypothetical prote	356	120	3.8	458	2	T31631	hypothetical prote
284	124.5	4.0	1223	2	B88451	protein K10D2.1 li	357	120	3.8	892	2	T09071	SH3 domains-conta
285	124.5	4.0	2176	2	T13806	toucan gene protei	358	120	3.8	962	2	T04124	receptor-like prot
286	124	4.0	433	2	S35047	conserved hypochet	359	120	3.8	1126	2	T20801	hypothetical prote
287	124	4.0	543	2	T43556	mucin JUD7 - human	360	120	3.8	1224	2	T40765	web1 protein homol
288	124	4.0	574	2	T43556	Wiskott-Aldrich sy	361	119.5	3.8	267	2	S08314	cell wall glycopro
289	124	4.0	605	2	AG0123	probable antigenic	362	119.5	3.8	479	1	A31753	transcription fact
290	124	4.0	729	2	E70803	hypothetical prote	363	119.5	3.8	660	2	T15569	receptor protein k
291	124	4.0	766	2	B85440	receptor kinase-1i	364	119.5	3.8	1048	1	XPBEA9	large structural p
292	124	4.0	978	2	E66787	protein T4O12.5 li	365	119.5	3.8	1079	2	C96772	probable receptor
293	124	4.0	1011	2	T45718	receptor-kinase 1i	366	119.5	3.8	1166	2	F96558	protein P20N2.4 li
294	124	4.0	1472	2	B54774	ATP binding caset	367	119.5	3.8	1400	2	B70963	hypothetical prote
295	124	4.0	4135	2	T42629	tenascin-X - bovin	368	119.5	3.8	1596	2	A35927	190K DNA-binding p
296	123.5	3.9	380	2	T01281	probable leucine-r	369	119.5	3.8	1643	2	T14274	versican precursor
297	123.5	3.9	492	2	F86263	hypothetical prote	370	119	3.8	164	2	I53641	mucin 5AC - human
298	123.5	3.9	656	2	AE1479	probable cell surf	371	119	3.8	352	2	S49299	AW0172 protein -
299	123.5	3.9	690	2	T41296	probable alcohol d	372	119	3.8	424	2	S27783	hypothetical prote
300	123	3.9	528	2	T15198	hypothetical prote	373	119	3.8	650	2	C75557	hypothetical prote
301	123	3.9	574	2	T38819	wiskot-aldrich sy	374	119	3.8	651	2	T42644	hypothetical prote
302	123	3.9	888	2	S23065	ufo protein - mous	375	119	3.8	660	1	Q0E83	BHLF1 protein - hu
303	123	3.9	1072	2	A37127	microtubule-associ	376	119	3.8	808	2	T23129	hypothetical prote
304	123	3.9	2591	2	T030288	pristinamycin I sy	377	119	3.8	864	2	D84740	hypothetical prote
305	122.5	3.9	303	2	S28264	hydroxyproline-ric	378	119	3.8	1006	2	T42731	atropin-1 related
306	122.5	3.9	415	2	T13435	hypothetical prote	379	119	3.8	1045	2	T41119	internalin-relate
307	122.5	3.9	592	2	D70863	hypothetical prote	380	118.5	3.8	222	2	H86711	hypothetical prote
308	122.5	3.9	699	2	T05425	extensin homolog F	381	118.5	3.8	400	1	A39822	leukostatin precur
309	122.5	3.9	809	2	B84634	probable receptor-	382	118.5	3.8	677	2	E70722	hypothetical prote
310	122.5	3.9	845	2	T12537	hypothetical prote	383	118.5	3.8	751	2	AC2098	hypothetical prote
311	122.5	3.9	1016	2	T30553	disease resistance	384	118.5	3.8	869	2	A71400	probable disease r
312	122.5	3.9	2444	2	A54849	collagen alpha 1(V	385	118.5	3.8	883	2	S57653	brevian precursor
313	122	3.9	298	2	UC4130	osteoeglycin precu	386	118.5	3.8	988	2	T45717	receptor-kinase 1i
314	122	3.9	326	2	T24722	hypothetical prote	387	118.5	3.8	1173	2	T25893	hypothetical prote
315	122	3.9	596	2	AE1515	internalin like pr	388	118.5	3.8	1356	2	A45445	janusin precursor,
316	122	3.9	623	2	T19876	hypothetical prote	389	118.5	3.8	1607	2	T02837	long chain fatty a
317	122	3.9	672	2	B84782	probable receptor-	390	118	3.8	294	2	A37232	mucin, tracheal (A
318	122	3.9	715	2	G86239	protein P20B24.6 l	391	118	3.8	599	2	T10798	muin, tracheal (A
319	122	3.9	719	2	T47727	hypothetical prote	392	118	3.8	667	2	S74254	homeotic protein s
320	122	3.9	921	2	B86234	hypothetical prote	393	118	3.8	823	2	AD1935	general secretion
321	122	3.9	992	2	T05335	hypothetical prote	394	118	3.8	1134	1	JN0711	protein-tyrosine k

395	118	3.8	2471	2	A49128	cell-fate determin	468	114	3.6	378	2	S00842	leukosialin precu
396	117.5	3.7	473	2	D85041	hypothetical prote	469	114	3.6	413	1	A34888	transcription fact
397	117.5	3.7	624	2	A55576	collagen alpha 2(X	470	114	3.6	555	1	S20100	mullerian inhibiti
398	117.5	3.7	660	2	JW0067	chitinase (EC 3.2	471	114	3.6	596	2	T29695	hypothetical prote
399	117.5	3.7	996	2	T10725	protein kinase Xa2	472	114	3.6	633	2	S62057	proline-rich prote
400	117.5	3.7	1075	2	D70568	hypothetical prote	473	114	3.6	634	2	T00388	hypothetical prote
401	117.5	3.7	1706	2	I84499	zinc finger protei	474	114	3.6	656	2	E75468	hypothetical prote
402	117	3.7	431	2	T27904	hypothetical prote	475	114	3.6	768	2	A42755	P-selectin precurs
403	117	3.7	655	1	A46688	hepatocyte growth	476	114	3.6	1290	2	T00018	period protein hom
404	117	3.7	670	2	H96707	probable receptor	477	114	3.6	2225	2	T26063	hypothetical prote
405	117	3.7	678	2	JC4245	transcription fact	478	113.5	3.6	317	2	S55316	mucin (clone PGM-2
406	117	3.7	743	2	C84633	probable disease r	479	113.5	3.6	330	2	T46256	brevican - human (
407	117	3.7	801	2	T29018	hypothetical prote	480	113.5	3.6	538	2	T01102	disease resistance
408	117	3.7	1007	2	C84668	probable receptor-	481	113.5	3.6	896	2	B43817	transforming prote
409	117	3.7	1009	2	D75399	probable penicilli	482	113.5	3.6	907	2	A86460	99.9K hypothetical
410	117	3.7	1328	2	T43060	agrin - electric r	483	113.5	3.6	938	1	QOB524	nuclear antigen EB
411	117	3.7	1450	2	T30273	hypothetical prote	484	113.5	3.6	1286	2	T33476	hypothetical prote
412	117	3.7	1574	2	T13954	MEGF6 protein - ra	485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
413	117	3.7	2082	2	T37056	probable multi-dom	486	113.5	3.6	2911	2	T20566	hypothetical prote
414	117	3.7	2232	2	T34434	hypothetical prote	487	113	3.6	371	2	T49908	hypothetical prote
415	116.5	3.7	279	2	S53363	mucin 5AC (clone J	488	113	3.6	377	2	A48018	mucin 7 precursor,
416	116.5	3.7	439	2	S51939	chitinase (EC 3.2.	489	113	3.6	382	2	E84527	hypothetical prote
417	116.5	3.7	621	2	I38467	low density lipopr	490	113	3.6	419	2	A90888	hypothetical prote
418	116.5	3.7	787	2	T27632	hypothetical prote	491	113	3.6	419	2	H85729	hypothetical prote
419	116.5	3.7	794	2	T27632	hypothetical prote	492	113	3.6	603	2	A75373	probable N-acetylm
420	116.5	3.7	828	2	A88860	protein ZC518.3 [i	493	113	3.6	979	2	A35913	regulatory factor
421	116.5	3.7	1048	2	T31425	C-terminal domain-	494	113	3.6	982	2	A53253	microtubule-associ
422	116.5	3.7	1446	1	A45344	immediate-early pr	495	113	3.6	1002	2	T46033	receptor protein k
423	116.5	3.7	2229	2	T16199	hypothetical prote	496	113	3.6	1025	2	T45847	receptor protein k
424	116	3.7	292	2	S24169	mucin - rat	497	113	3.6	1069	2	S27922	nuclear antigen EB
425	116	3.7	652	2	A71753	repellent protein	498	113	3.6	1247	2	T42209	neural plakophilin
426	116	3.7	660	2	AH2348	hypothetical prote	499	113	3.6	1343	2	AF0611	cell division prot
427	116	3.7	729	2	F86308	Similar to disease	500	113	3.6	2688	2	I49477	alpha-A-crystallin
428	116	3.7	771	2	T02565	disease resistance	501	113	3.6	3381	2	T42389	versican precursor
429	116	3.7	808	2	B97303	hypothetical prote	502	112.5	3.6	347	2	S10571	mucin 1 precursor,
430	116	3.7	845	2	T07039	Hcr9-0 protein - t	503	112.5	3.6	581	2	G96811	unknown protein T1
431	116	3.7	907	2	A24938	hypothetical T2 pr	504	112.5	3.6	731	2	B86369	hypothetical prote
432	116	3.7	1291	2	T00019	period protein hom	505	112.5	3.6	1075	2	A57377	transcription fact
433	116	3.7	1494	2	T14355	protein-tyrosine-p	506	112.5	3.6	1237	2	AC1583	transcription fact
434	116	3.7	1840	2	T30250	Gri protein - mous	507	112.5	3.6	1680	2	T01367	hypothetical prote
435	116	3.7	2531	2	A46043	notch-1 protein -	508	112.5	3.6	2479	2	F87386	conserved hypotet
436	116	3.7	2555	2	A40043	notch protein homo	509	112.5	3.6	4006	2	T09070	probable tenascin
437	116	3.7	2774	2	A43359	microtubule-associ	510	112	3.6	241	2	S32359	glial growth facto
438	115.5	3.7	322	2	A53715	apomucin precursor	511	112	3.6	252	2	T01787	thyrotropin recept
439	115.5	3.7	513	2	AC3061	hypothetical prote	512	112	3.6	253	1	JC1319	thyrotropin recept
440	115.5	3.7	513	2	D98225	hypothetical prote	513	112	3.6	285	2	A41826	probable pheromone
441	115.5	3.7	528	2	I47141	gastric mucin (clo	514	112	3.6	383	2	S53716	transcription fact
442	115.5	3.7	696	2	T42659	hypothetical prote	515	112	3.6	413	2	A48756	delta-like homeoti
443	115.5	3.7	805	2	T49385	hypothetical prote	516	112	3.6	704	2	AE2107	serine/threonine k
444	115.5	3.7	946	2	S27921	nuclear antigen EB	517	112	3.6	731	2	T04455	hypothetical prote
445	115.5	3.7	1093	2	I38533	AF17 protein - hum	518	112	3.6	742	2	F84643	hypothetical prote
446	115.5	3.7	1268	2	S52781	neurocan - mouse	519	112	3.6	764	1	QRHURH	thyrotropin recept
447	115.5	3.7	1460	1	EDBE1F	immediate-early pr	520	112	3.6	883	2	S49126	brevican precursor
448	115.5	3.7	2214	2	T16305	hypothetical prote	521	112	3.6	960	2	G84652	probable receptor-
449	115.5	3.7	3421	1	WZBBB6	367K tegument prot	522	112	3.6	990	2	T03784	probable receptor
450	115	3.7	404	2	T08549	hypothetical prote	523	112	3.6	1032	2	T34433	hypothetical prote
451	115	3.7	451	2	S74728	hypothetical prote	524	112	3.6	1289	2	AB2217	hypothetical prote
452	115	3.7	461	2	T10741	extensin-like prot	525	111.5	3.6	224	2	D72861	hypothetical prote
453	115	3.7	479	1	T25452	transcription fact	526	111.5	3.6	383	2	S32975	Gene BCRF2 protein
454	115	3.7	539	2	AH1216	internalin, probab	527	111.5	3.6	478	1	I47154	transcription fact
455	115	3.7	766	2	T01817	hypothetical prote	528	111.5	3.6	645	2	T05251	transcription fact
456	115	3.7	838	2	T08423	Axin homolog Axil	529	111.5	3.6	649	2	T46500	hypothetical prote
457	115	3.7	980	2	T05414	protein kinase hom	530	111.5	3.6	1047	2	A55617	masquerade precurs
458	115	3.7	1133	2	B86308	hypothetical prote	531	111.5	3.6	1253	2	T45787	disease resistance
459	115	3.7	1220	2	A56136	Jagged protein pre	532	111.5	3.6	1298	1	EDBE75	immediate-early pr
460	115	3.7	2415	1	A39086	aggreacan precursor	533	111.5	3.6	1353	1	JH0675	restrictin precurs
461	114.5	3.7	328	2	JQ0985	hydroxyproline-ric	534	111.5	3.6	2649	2	T51023	hypothetical prote
462	114.5	3.7	409	2	T11743	p47 protein - pig	535	111	3.5	274	2	JC8063	heart-restricted l
463	114.5	3.7	505	2	AC1469	internalin like pr	536	111	3.5	478	2	H86459	hypothetical prote
464	114.5	3.7	606	2	T51880	hypothetical prote	537	111	3.5	509	2	T05260	probable disease r
465	114.5	3.7	627	2	T27123	hypothetical prote	538	111	3.5	518	2	S50465	PAC2 protein - yea
466	114.5	3.7	638	2	T05606	protein kinase hom	539	111	3.5	548	2	E70546	hypothetical prote
467	114	3.6	218	2	T01104	disease resistance	540	111	3.5	603	2	S28941	coagulation factor

541	111	3.5	610	2	S35049	614	109	3.5	2809	2	T30213	G-cadherin - sea u
542	111	3.5	620	1	T50150	615	108.5	3.5	308	2	UC7125	epidermal growth f
543	111	3.5	699	1	QRHUT	616	108.5	3.5	389	2	S27200	proline-rich prote
544	111	3.5	853	2	T17461	617	108.5	3.5	402	2	A84581	probable disease r
545	111	3.5	932	2	T21338	618	108.5	3.5	418	2	T15142	hypothetical prote
546	111	3.5	984	2	T48216	619	108.5	3.5	499	2	A11107	internalin E [impo
547	111	3.5	1221	1	T38902	620	108.5	3.5	514	2	H70699	probable ppp prote
548	111	3.5	2524	1	A35844	621	108.5	3.5	548	1	T37577	islet cell antigen
549	110.5	3.5	359	2	C55066	622	108.5	3.5	622	2	A45155	mucin FIM-C.1 - Af
550	110.5	3.5	421	2	A60058	623	108.5	3.5	698	2	T39713	ce1b protein - Agr
551	110.5	3.5	512	2	G86459	624	108.5	3.5	710	1	QOBE22	membrane antigen g
552	110.5	3.5	525	1	A58674	625	108.5	3.5	740	2	B84741	hypothetical prote
553	110.5	3.5	533	2	T07970	626	108.5	3.5	756	2	G86308	Similar to disease
554	110.5	3.5	565	2	JE0338	627	108.5	3.5	783	1	A35956	thyrotropin recept
555	110.5	3.5	684	2	T01267	628	108.5	3.5	793	1	A38637	Ras interactor RIN
556	110.5	3.5	803	1	S35695	629	108.5	3.5	825	1	A40026	neurotrophin-3 rec
557	110.5	3.5	815	2	B56708	630	108.5	3.5	855	2	C82983	hypothetical prote
558	110.5	3.5	855	2	T07015	631	108.5	3.5	1011	2	C84524	probable disease r
559	110.5	3.5	872	2	S33015	632	108.5	3.5	1125	2	B41206	microtubule-associ
560	110.5	3.5	992	2	A31666	633	108.5	3.5	1176	2	T49482	hypothetical prote
561	110.5	3.5	1207	2	T00378	634	108.5	3.5	1184	2	A301763	atrophin-1 - human
562	110.5	3.5	1295	2	A32901	635	108.5	3.5	1344	1	A35175	mucin 1 precursor,
563	110.5	3.5	1344	2	T14316	636	108.5	3.5	1357	2	T29265	hypothetical prote
564	110.5	3.5	1346	2	T17412	637	108.5	3.5	1487	2	T02850	hypothetical prote
565	110.5	3.5	1736	2	T00391	638	108.5	3.5	3707	2	S18252	heparan sulfate pr
566	110.5	3.5	2476	2	T34022	639	108	3.4	348	2	AG0752	hypothetical 35.5k
567	110.5	3.5	275	2	T51437	640	108	3.4	409	2	JQ0431	flagellar hook-len
568	110	3.5	391	2	T04609	641	108	3.4	511	1	VGBE1K	glycoprotein C - h
569	110	3.5	549	2	S32987	642	108	3.4	542	2	T39540	chitinase (EC 3.2,
570	110	3.5	591	2	D84889	643	108	3.4	544	2	T17547	proline-rich prote
571	110	3.5	708	2	D96711	644	108	3.4	550	2	T36746	probable serine/th
572	110	3.5	719	2	T02154	645	108	3.4	638	1	XXAV	dihydrolipoamide S
573	110	3.5	764	2	I48882	646	108	3.4	741	2	T05250	probable disease r
574	110	3.5	846	2	H70599	647	108	3.4	862	2	S43922	veriscan - pig-tai
575	110	3.5	846	2	T21700	648	108	3.4	996	2	JB0237	apolipoprotein E r
576	110	3.5	951	2	A96770	649	108	3.4	1017	2	T31354	probable potassium
577	110	3.5	1123	2	D96756	650	108	3.4	1217	2	T51140	disease resistance
578	110	3.5	1483	2	E86143	651	108	3.4	1217	2	T51141	disease resistance
579	110	3.5	1711	1	A55148	652	108	3.4	2783	1	A41948	alpha-fetoprotein
580	110	3.5	2703	1	A24420	653	108	3.4	3511	2	A59295	unconventional myo
581	110	3.5	2715	2	T13049	654	108	3.4	4613	2	T17409	polyketide synthas
582	110	3.5	3942	2	T42730	655	108	3.4	7576	2	T17428	FK506 polyketide s
583	109.5	3.5	213	2	A86228	656	107.5	3.4	363	2	H87702	hypothetical prote
584	109.5	3.5	279	2	T10361	657	107.5	3.4	369	2	S20500	hydroxyproline-ric
585	109.5	3.5	318	2	T29479	658	107.5	3.4	414	2	G66770	hypothetical prote
586	109.5	3.5	428	2	E71415	659	107.5	3.4	427	2	S74211	PAS-6/7 protein pr
587	109.5	3.5	473	2	S36553	660	107.5	3.4	536	2	H71563	hypothetical prote
588	109.5	3.5	507	2	T44768	661	107.5	3.4	604	2	S25203	srnr protein - Str
589	109.5	3.5	538	2	S57459	662	107.5	3.4	655	2	G96524	protein TIM5.9 [l
590	109.5	3.5	558	2	JC5878	663	107.5	3.4	832	2	A31246	neurogenic repetit
591	109.5	3.5	583	1	S22544	664	107.5	3.4	880	2	S00670	cellulose synthase
592	109.5	3.5	612	2	T17633	665	107.5	3.4	881	2	B98320	neurogenic repetit
593	109.5	3.5	825	2	A55178	666	107.5	3.4	1009	2	T45645	receptor kinase-11
594	109.5	3.5	839	1	T173632	667	107.5	3.4	1099	2	A56155	tumor suppressor p
595	109.5	3.5	874	2	E97302	668	107.5	3.4	1206	2	S24407	formin isoform IV
596	109.5	3.5	878	2	T21621	669	107.5	3.4	1324	2	S52863	DNA-binding protei
597	109.5	3.5	954	2	T19765	670	107.5	3.4	1468	2	T151515	formin - mouse
598	109.5	3.5	1299	2	T47182	671	107.5	3.4	3534	2	T42567	tegument protein 2
599	109.5	3.5	1776	1	RKWPYM	672	107	3.4	176	1	A46606	platelet glycoprot
600	109.5	3.5	2531	2	T31070	673	107	3.4	228	2	S53504	extensin-like prot
601	109.5	3.5	2717	2	A34203	674	107	3.4	273	2	A28512	fibronectin - chic
602	109	3.5	379	2	T05441	675	107	3.4	354	2	A48931	transmembrane glyc
603	109	3.5	379	2	D85257	676	107	3.4	358	1	WMBE38	infected cell prot
604	109	3.5	395	2	I52842	677	107	3.4	416	1	SKX1AG	dermal gland prote
605	109	3.5	395	2	A43545	678	107	3.4	447	2	A39321	mucin - rat (fragm
606	109	3.5	403	2	S52796	679	107	3.4	452	2	C41602	transcription fact
607	109	3.5	426	2	J01696	680	107	3.4	518	2	F75460	hypothetical prote
608	109	3.5	431	2	T04868	681	107	3.4	615	1	KFHU12	coagulation factor
609	109	3.5	437	2	A54595	682	107	3.4	650	2	S59630	dysregglycan alpha
610	109	3.5	598	2	C96756	683	107	3.4	840	1	S69204	phenomene response
611	109	3.5	613	2	T42671	684	107	3.4	915	2	T12526	hypothetical prote
612	109	3.5	833	2	S19087	685	107	3.4	1063	1	GNWVR4	structural polypro
613	109	3.5	1611	2	T38236	686	107	3.4	1376	2	G00043	osteonidogen - hum

687	107	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	3.4	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T03561	scythe protein - A
689	107	3.4	7463	2	T36248	CDA peptide synthe	762	105	3.3	1136	1	S57845	protein-tyrosine k
690	106.5	3.4	304	2	A32993	transcription fact	763	105	3.3	1456	2	T01397	LTR gag/pol polypr
691	106.5	3.4	353	2	A41558	N-syndecan - rat (	764	105	3.3	1858	2	D75489	hypothetical prote
692	106.5	3.4	505	2	B46629	mucin 6, gastric (	765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	3.4	509	2	D86911	conserved hypotet	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	3.4	509	2	T10013	probable phosphor	767	105	3.3	2409	1	A60979	vesican precursor
695	106.5	3.4	517	2	AD1570	internalin, probab	768	105	3.3	2769	1	UIBO	thryoglobulin prec
696	106.5	3.4	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	leucine rich repea
697	106.5	3.4	827	2	AC2963	ceLB protein (mpo	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	3.4	925	2	H96638	protein TfR9.20 li	771	104.5	3.3	464	2	T35944	probable hydrolyti
699	106.5	3.4	998	2	C75489	conserved hypotet	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	3.4	1003	2	T13856	ksr protein - frui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	3.4	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	3.4	1184	2	S50832	atrophin-1 - human	775	104.5	3.3	700	2	A42395	lutropin receptor
703	106.5	3.4	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	3.4	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	probable ABC trans
705	106.5	3.4	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	hypothetical prote
706	106.5	3.4	2090	2	S26058	probable transform	779	104.5	3.3	755	2	T20950	hypothetical prote
707	106.5	3.4	2453	2	S60254	nuclear receptor C	780	104.5	3.3	909	1	QRXL1	LDL receptor 1 pre
708	106	3.4	135	2	T49396	AtGRP4 - Arabidops	781	104.5	3.3	960	1	S28262	kinesin-related pr
709	106	3.4	167	2	A33532	mucin SMUC-40 - hu	782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
710	106	3.4	216	2	I51920	mucin - rhesus mac	783	104.5	3.3	1194	2	E96624	hypothetical prote
711	106	3.4	287	2	S65765	chitinase (EC 3.2.	784	104.5	3.3	1241	2	T37190	nephrin - human
712	106	3.4	405	2	S78691	flagellar hook-len	785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
713	106	3.4	431	2	S47538	acrosin (EC 3.4.21	786	104.5	3.3	1851	2	T19964	hypothetical prote
714	106	3.4	435	2	D41602	transcription fact	787	104.5	3.3	1898	2	S46216	leukocyte antigen-
715	106	3.4	443	2	B39794	transcription fact	788	104.5	3.3	2117	2	T36180	CDA peptide synthe
716	106	3.4	449	2	A24993	cellulase (EC 3.2.	789	104	3.3	232	2	A60095	larval glue protei
717	106	3.4	567	2	A45977	Rab geranylgeranyl	790	104	3.3	306	2	I49139	lymphotoxin-beta -
718	106	3.4	666	2	B70803	hypothetical prote	791	104	3.3	318	2	B64900	hypothetical prote
719	106	3.4	701	2	D48613	gag polypeptide -	792	104	3.3	326	2	A46576	CD68 homolog macro
720	106	3.4	818	2	T01105	disease resistance	793	104	3.3	332	2	S43988	protein phosphatas
721	106	3.4	822	2	T51049	related to nucleol	794	104	3.3	360	2	S68209	sds22 protein homo
722	106	3.4	850	2	S56012	gastric mucin MUC5	795	104	3.3	365	2	A39481	serum response fac
723	106	3.4	901	2	A49227	sialidase - Actino	796	104	3.3	426	2	D88103	protein W10211.6 [
724	106	3.4	914	2	T17233	hypothetical prote	797	104	3.3	440	2	I49681	glyceraldhyde-3-p
725	106	3.4	1064	2	A40136	fibropellin Ia - s	798	104	3.3	470	2	S36536	l2 protein - human
726	106	3.4	1603	2	A48613	gag/pol polyprotei	799	104	3.3	537	2	A46611	myosin-binding pro
727	106	3.4	1958	2	B40505	hypothetical prote	800	104	3.3	538	2	S65764	chitinase (EC 3.2.
728	106	3.4	2554	1	TVFF7L	kinase-related pro	801	104	3.3	593	2	S49525	glycoprotein G - s
729	106	3.4	3938	2	T42761	Bassoon protein -	802	104	3.3	712	1	I46031	gelatinase B (EC 3
730	105.5	3.4	395	2	T01392	leucine-rich repea	803	104	3.3	895	2	S20582	dystrophin-associa
731	105.5	3.4	486	2	A41537	DNA-binding protei	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	3.4	510	2	A42750	insulinoma-associa	805	104	3.3	1045	2	T16275	hypothetical prote
733	105.5	3.4	668	2	T05257	probable disease r	806	104	3.3	1547	2	T28657	blackjack protein,
734	105.5	3.4	688	2	T04568	protein kinase hom	807	104	3.3	1575	2	S68448	synaptotagmin, 170K
735	105.5	3.4	695	2	S62400	amphiphysin (clone	808	104	3.3	1711	2	T31337	1,4-beta-glucanase
736	105.5	3.4	722	2	T13078	KIAA0992 protein -	809	104	3.3	1744	2	A54970	tensin, cardiac mu
737	105.5	3.4	780	2	A48143	HF-1 regulatory el	810	104	3.3	3507	2	T34513	hypothetical prote
738	105.5	3.4	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	platelet glycoprot
739	105.5	3.4	1132	2	A35098	MHC class III hist	812	103.5	3.3	264	2	PQ0478	pistil extensin-li
740	105.5	3.4	1172	2	T00065	hypothetical prote	813	103.5	3.3	281	2	D70845	hypothetical prote
741	105.5	3.4	1621	2	T15264	hypothetical prote	814	103.5	3.3	393	2	PQ0479	pistil extensin-li
742	105.5	3.4	1712	2	A38261	masking protein pr	815	103.5	3.3	411	1	I55604	platelet glycoprot
743	105.5	3.4	1839	1	RRWEM	genome polypeptid	816	103.5	3.3	419	2	T49292	hypothetical prote
744	105.5	3.4	2477	2	S14428	fibronectin precur	817	103.5	3.3	444	1	A39794	transcription fact
745	105.5	3.4	3033	1	JQ1303	genome polypeptid	818	103.5	3.3	489	2	F75591	p49 secreted prote
746	105	3.3	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	nicotinic acetylch
747	105	3.3	422	2	I37891	interleukin-11 rec	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	3.3	454	2	E75291	probable cell wall	821	103.5	3.3	889	2	F96637	hypothetical prote
749	105	3.3	460	2	T33110	hypothetical prote	822	103.5	3.3	889	2	T20123	hypothetical prote
750	105	3.3	486	1	A57601	transcription fact	823	103.5	3.3	968	2	T00353	hypothetical prote
751	105	3.3	511	1	VGBERF4	glycoprotein C - h	824	103.5	3.3	975	2	I48974	regulatory protein t
752	105	3.3	566	2	T34842	probable transferr	825	103.5	3.3	980	2	S54986	receptor-protein
753	105	3.3	620	2	A70525	hypothetical prote	826	103.5	3.3	1020	2	A29355	fibronectin - chic
754	105	3.3	658	2	T08153	cysteine proteinas	827	103.5	3.3	1144	2	A54810	hypothetical prote
755	105	3.3	730	2	JC1456	gelatinase B (EC 3	828	103.5	3.3	1171	2	T35548	C-terminal domain-
756	105	3.3	764	2	JC5643	thyroid stimulat	829	103.5	3.3	1268	2	T31420	protein T7N9.24 [i
757	105	3.3	847	1	A53800	mixed-lineage prot	830	103.5	3.3	1590	2	B86398	collagen alpha 1(X
758	105	3.3	895	2	I54343	dystroglycan - hum	831	103.5	3.3	1603	2	S23810	transcription acti
759	105	3.3	976	2	A36355	protein-tyrosine k	832	103.5	3.3	1638	2	A42091	



833	103.5	3.3	1733	1	B45344	probable nuclear a
834	103.5	3.3	3739	2	T17410	polyketide synthas
835	103	3.3	168	2	S52994	arabinogalactan-11
836	103	3.3	191	2	B84740	hypothetical prote
837	103	3.3	227	2	T27905	hypothetical prote
838	103	3.3	263	2	S01360	salivary glue prot
839	103	3.3	362	2	A44083	meg protein - Mare
840	103	3.3	367	2	AC1328	internalin protein
841	103	3.3	379	2	T16213	APX-1 protein homo
842	103	3.3	394	2	C84905	probable extensin
843	103	3.3	515	2	F70904	hypothetical prote
844	103	3.3	535	1	S76953	protein kinase (EC
845	103	3.3	550	2	G70597	probable proteinas
846	103	3.3	575	2	UG0181	Xll22 protein - hu
847	103	3.3	611	2	B86387	unknown protein [i
848	103	3.3	648	2	T35120	hypothetical prote
849	103	3.3	701	2	F48613	gag polyprotein -
850	103	3.3	793	2	JC7390	thyroid stimulatn
851	103	3.3	799	1	TVR1TB	nerve growth facto
852	103	3.3	813	2	T04313	protein kinase Xa2
853	103	3.3	851	2	S67285	NUDI protein - yea
854	103	3.3	863	2	A55173	cf-9 protein precu
855	103	3.3	915	2	S36327	clathrin assembly
856	103	3.3	1040	2	T29092	TSG-22 protein hom
857	103	3.3	1121	2	A82809	exodeoxyribonuclea
858	103	3.3	1199	2	A40670	nuclear envelope p
859	103	3.3	1201	2	G86441	unknown protein [i
860	103	3.3	1375	2	T33369	hypothetical prote
861	103	3.3	1440	2	A39808	proteoglycan core
862	103	3.3	1541	2	T02831	AAA protein L4171.
863	103	3.3	1894	2	C54689	protein-tyrosine-p
864	103	3.3	2207	1	GNNY5P	genome polyprotein
865	103	3.3	2481	2	A43908	fibronectin - Afri
866	103	3.3	3133	2	S52093	hemocytin - silkw
867	102.5	3.3	217	2	S01358	salivary glue prot
868	102.5	3.3	252	2	T04739	hypothetical prote
869	102.5	3.3	316	2	T31880	hypothetical prote
870	102.5	3.3	338	2	I53043	transforming prote
871	102.5	3.3	352	2	S17313	transcription fact
872	102.5	3.3	371	2	F70555	hypothetical prote
873	102.5	3.3	379	2	S31719	proline-rich prote
874	102.5	3.3	383	2	B86272	protein Fl6A14.12
875	102.5	3.3	385	2	S53718	homocit protein d
876	102.5	3.3	385	2	A54785	predipocyte facto
877	102.5	3.3	421	2	T30709	core protein homol
878	102.5	3.3	507	1	A32385	erythropoietin rec
879	102.5	3.3	627	2	D75393	serine proteinase,
880	102.5	3.3	674	2	T05264	probable serine/th
881	102.5	3.3	706	2	E30411	synapsin Ia - bov
882	102.5	3.3	730	1	I52580	gelatinase B (EC 3
883	102.5	3.3	760	1	S07896	transcription fact
884	102.5	3.3	904	2	T46170	disease resistance
885	102.5	3.3	907	2	E96636	hypothetical prote
886	102.5	3.3	942	1	JQ1674	protein kinase TMK
887	102.5	3.3	964	2	JC5545	integrin beta-4 pr
888	102.5	3.3	1013	2	T46422	hypothetical prote
889	102.5	3.3	1115	1	TJMSNL	neural cell adhesi
890	102.5	3.3	1223	2	T15316	hypothetical prote
891	102.5	3.3	1350	2	G36793	hypothetical prote
892	102.5	3.3	1367	1	S48478	glucan 1,4-alpha-g
893	102.5	3.3	1678	2	T35547	hypothetical prote
894	102.5	3.3	1779	2	T31085	xylanase - Caldice
895	102.5	3.3	1813	2	T30564	resistance protein
896	102.5	3.3	1863	2	S46217	protein-tyrosine-p
897	102.5	3.3	1875	2	A36429	integrin beta-4 ch
898	102.5	3.3	2207	2	S09553	genome polyprotein
899	102	3.3	301	2	JQ1663	hybrid poline-ric
900	102	3.3	307	2	S35779	ribosome-binding p
901	102	3.3	317	2	A28996	proline-rich prote
902	102	3.3	353	2	B36963	bcsA 5'-region pro
903	102	3.3	413	2	T49545	hypothetical prote
904	102	3.3	532	2	S74453	hypothetical prote
905	102	3.3	554	1	FGHUMP	macrophage colony-
906	102	3.3	567	2	JC5538	Rab geranylgeranyl
907	102	3.3	585	1	B70747	probable serine/th
908	102	3.3	650	2	B87791	protein B0207.1 [i
909	102	3.3	670	2	S22293	zinc finger protei
910	102	3.3	715	2	T12534	hypothetical prote
911	102	3.3	732	2	I48324	DELTA-like 1 - mou
912	102	3.3	728	2	D86278	hypothetical prote
913	102	3.3	800	2	B84646	probable receptor-
914	102	3.3	866	1	A35782	cytokine receptor
915	102	3.3	923	1	A39596	progesterone recep
916	102	3.3	963	2	A55926	DNA binding protei
917	102	3.3	1008	2	T04462	hypothetical prote
918	102	3.3	1021	2	H75423	hypothetical prote
919	102	3.3	1032	2	D83637	serine/threonine p
920	102	3.3	1052	2	B49120	protein-tyrosine k
921	102	3.3	1069	2	D85383	hypothetical prote
922	102	3.3	1137	2	A86335	T20H2.9 protein -
923	102	3.3	1166	2	T13958	synGAP-D1 protein
924	102	3.3	1249	2	T14270	Ras-GTPase activat
925	102	3.3	1293	2	T14259	Ras GTPase-activat
926	102	3.3	1692	2	A33988	adenylate cyclase
927	102	3.3	1985	2	S19151	hypothetical prote
928	102	3.3	2218	2	B84683	hypothetical prote
929	102	3.3	2437	2	S42612	transmembrane prot
930	102	3.3	2440	2	S39162	transcription coac
931	102	3.3	2441	2	S39161	CREB-binding prote
932	102	3.3	3124	2	A40020	collagen alpha 1(X
933	102	3.3	5147	1	IJFPTM	cadherin-related t
934	101.5	3.2	98	2	S53367	much 5AC (clone M
935	101.5	3.2	173	2	T47176	hypothetical prote
936	101.5	3.2	244	2	A40428	nonspecific cross-
937	101.5	3.2	372	2	T29359	hypothetical prote
938	101.5	3.2	409	2	T43599	YOP targeted effec
939	101.5	3.2	547	2	B56573	nuclear pore compl
940	101.5	3.2	654	2	C87587	hypothetical prote
941	101.5	3.2	657	2	B84869	probable Srf6 prot
942	101.5	3.2	710	2	T44753	hypothetical prote
943	101.5	3.2	728	2	I50719	C-Delta-1 - chicke
944	101.5	3.2	733	2	A87168	conserved hypochet
945	101.5	3.2	833	2	AF2089	hypothetical prote
946	101.5	3.2	869	2	A55384	transcription fact
947	101.5	3.2	921	2	S40495	collagen alpha 1(I
948	101.5	3.2	947	2	G86420	probable receptor-
949	101.5	3.2	977	2	I52657	seizure-related pr
950	101.5	3.2	984	1	A34076	protein-tyrosine k
951	101.5	3.2	1034	2	JC5569	serine proteinase
952	101.5	3.2	1039	2	A85096	hypothetical prote
953	101.5	3.2	1429	2	S06434	homeotic protein 1
954	101.5	3.2	1668	2	T13748	sex comb protein -
955	101.5	3.2	1733	2	S27939	tensin - chicken
956	101.5	3.2	4543	1	A53102	alpha-2-macroglobu
957	101	3.2	240	2	B24264	proline-rich prote
958	101	3.2	249	2	S72619	hypothetical prote
959	101	3.2	294	2	T34537	hypothetical prote
960	101	3.2	360	2	S25861	transcription fact
961	101	3.2	373	2	A44478	probable cell grow
962	101	3.2	401	2	A48423	engrailed homeodom
963	101	3.2	482	2	A44997	mezoote surface
964	101	3.2	492	2	B86911	probable penicilli
965	101	3.2	574	2	B87619	sensor histidine k
966	101	3.2	610	2	A28798	myosin-light-chain
967	101	3.2	613	2	A04997	dihydroliipoamide S
968	101	3.2	615	1	XXHU	hypothetical 69K p
969	101	3.2	628	2	JQ0110	hypothetical 69K p
970	101	3.2	681	2	D84648	probable disease r
971	101	3.2	671	2	T18263	S-layer protein -
972	101	3.2	700	2	D70951	transcription fact
973	101	3.2	739	2	I56187	transcription fact
974	101	3.2	796	2	T21460	hypothetical prote
975	101	3.2	846	1	Q088C3	HOKR1 protein - hu
976	101	3.2	1043	2	A56037	DNA-binding protei
977	101	3.2	1127	2	T32404	hypothetical prote
978	101	3.2	1257	2	S28764	neurocan precursor

979	101	3.2	1367	2	T33819	hypothetical prote	1052	99.5	3.2	352	2	S05500	Ig alpha-1 chain C
980	101	3.2	1513	2	A54895	mucin 2, intestina	1053	99.5	3.2	353	1	AIHU	Ig alpha-1 chain C
981	101	3.2	1792	2	A57075	tensin - chicken (	1054	99.5	3.2	353	2	S36438	EBP1 protein - hyd
982	101	3.2	2946	2	T15840	hypothetical prote	1055	99.5	3.2	375	1	TGHUM4	monocyte surface g
983	101	3.2	3176	2	CGHU3A	collagen alpha 3(V	1056	99.5	3.2	383	1	VGBEKG	glycoprotein precu
984	100.5	3.2	138	2	D96715	protein F4N2.10 [i	1057	99.5	3.2	387	2	B49175	Notch A protein -
985	100.5	3.2	262	2	T33408	hypothetical prote	1058	99.5	3.2	392	2	B48423	homeotic protein e
986	100.5	3.2	262	2	E88400	protein H34I24.2 [	1059	99.5	3.2	393	1	VGBED2	glycoprotein D - h
987	100.5	3.2	269	2	T26957	hypothetical prote	1060	99.5	3.2	420	2	T46910	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote	1061	99.5	3.2	451	2	JC4199	heat-shock protein
989	100.5	3.2	283	2	E88597	protein Y4YD3B.6 [	1062	99.5	3.2	476	1	C70986	probable serine/th
990	100.5	3.2	314	2	T48514	hypothetical prote	1063	99.5	3.2	491	2	F70599	probable pppA prot
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat	1064	99.5	3.2	530	2	S52215	hypothetical prote
992	100.5	3.2	401	2	S65138	glycoprotein antiq	1065	99.5	3.2	539	2	T28770	hypothetical prote
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy	1066	99.5	3.2	647	2	T43952	hypothetical prote
994	100.5	3.2	504	2	AG2373	hypothetical prote	1067	99.5	3.2	665	2	S62328	kinesin-like DNA b
995	100.5	3.2	504	2	S56745	mucin (clone pGM31	1068	99.5	3.2	702	2	A86383	76.4K protein kina
996	100.5	3.2	512	2	E59437	F02569_2 protein [	1069	99.5	3.2	802	2	T24293	hypothetical prote
997	100.5	3.2	597	2	TJQ0107	hypothetical 66K p	1070	99.5	3.2	851	2	AD1427	internalin, probab
998	100.5	3.2	677	2	T39713	zinc finger protei	1071	99.5	3.2	853	1	IJBONC	neural cell adhesi
999	100.5	3.2	798	2	T34248	hypothetical prote	1072	99.5	3.2	886	2	T35469	probable ATP /GTP-
1000	100.5	3.2	906	2	A43817	transforming prote	1073	99.5	3.2	903	2	T19209	probable protein k
1001	100.5	3.2	975	2	S33121	homeotic protein C	1074	99.5	3.2	949	2	T24294	hypothetical prote
1002	100.5	3.2	1024	2	T27631	hypothetical prote	1075	99.5	3.2	958	2	E82994	glycine cleavage s
1003	100.5	3.2	1030	2	H88859	protein ZC518.2 [i	1076	99.5	3.2	961	1	TSHUP4	thrombospondin 4 p
1004	100.5	3.2	1106	1	TVHUGL	transforming prote	1077	99.5	3.2	1013	2	T33470	hypothetical prote
1005	100.5	3.2	1131	2	F96662	hypothetical prote	1078	99.5	3.2	1016	2	T41720	hypothetical prote
1006	100.5	3.2	1138	1	S24066	protein-tyrosine k	1079	99.5	3.2	1056	2	A53767	mucin MUC5B, trach
1007	100.5	3.2	1220	2	T48928	disease resistance	1080	99.5	3.2	1122	2	T47424	hypothetical prote
1008	100.5	3.2	1273	2	S58782	SEC31 protein - ye	1081	99.5	3.2	1220	2	T06403	resistance complex
1009	100.5	3.2	1323	2	T30253	spalt protein - mo	1082	99.5	3.2	1390	2	T31353	polyprotein - Arab
1010	100.5	3.2	2327	2	T42630	aggreca - bovine	1083	99.5	3.2	1473	2	T31422	C-terminal domain-
1011	100.5	3.2	2562	2	T14266	Xin protein - chic	1084	99.5	3.2	1742	2	T17120	cellulase (EC 3.2.
1012	100.5	3.2	3562	2	A47171	chondroitin sulfat	1085	99.5	3.2	3869	2	A48205	All-1 protein +GTE
1013	100.5	3.2	458	1	S00657	apoptein(a) (EC	1086	99	3.2	134	2	PQ0476	pistil extensin-li
1014	100	3.2	230	2	A56210	neu differentiali	1087	99	3.2	214	2	T09854	proline-rich cell
1015	100	3.2	311	2	B86211	hypothetical prote	1088	99	3.2	307	1	GSFF3	salivary glue prot
1016	100	3.2	334	2	G02409	protein kinase C-b	1089	99	3.2	329	2	B41344	lutropin-choriogon
1017	100	3.2	366	2	S61796	T-cell-specific tr	1090	99	3.2	329	2	D41344	lutropin-choriogon
1018	100	3.2	367	2	A33950	yopM protein - Yer	1091	99	3.2	331	2	C41344	lutropin-choriogon
1019	100	3.2	474	2	S15921	protein TPX-VT3 -	1092	99	3.2	358	2	T01296	leucine-rich repea
1020	100	3.2	476	2	C39481	serum response fac	1093	99	3.2	415	1	A34170	acrosin (EC 3.4.21
1021	100	3.2	510	2	H48424	En/Spm-like transp	1094	99	3.2	428	2	S45361	LR47 protein - fr
1022	100	3.2	535	2	T17212	hypothetical prote	1095	99	3.2	447	2	T34992	probable lipoprote
1023	100	3.2	549	2	C87719	protein R119, 6 [im	1096	99	3.2	466	2	T06416	cysteine proteinas
1024	100	3.2	556	2	D70940	probable PPE prote	1097	99	3.2	511	2	AC0941	probable ABC trans
1025	100	3.2	562	2	S75308	DNA ligase (EC 6.5	1098	99	3.2	543	2	S25128	61K protein - Auto
1026	100	3.2	596	2	G75457	tetratricopeptide	1099	99	3.2	564	2	I53106	gene gli protein -
1027	100	3.2	628	2	S44138	polyadenylate-bind	1100	99	3.2	569	2	F75381	probable two-compo
1028	100	3.2	673	2	AF1143	internalin protein	1101	99	3.2	616	2	C75588	conserved hypoteth
1029	100	3.2	698	2	T51915	hypothetical prote	1102	99	3.2	638	2	T51383	receptor protein k
1030	100	3.2	698	2	T17261	hypothetical prote	1103	99	3.2	641	2	C84726	probable receptor-
1031	100	3.2	699	2	T09069	probable cAMP-resp	1104	99	3.2	686	2	F96542	probable protein k
1032	100	3.2	713	2	T44447	neuregulin-3 [impo	1105	99	3.2	696	2	A41344	lutropin-choriogon
1033	100	3.2	725	2	T01268	leucine-rich repea	1106	99	3.2	701	2	S61239	hypothetical prote
1034	100	3.2	756	2	C87432	hypothetical prote	1107	99	3.2	770	1	S30293	transcription fact
1035	100	3.2	776	2	A46583	neuroendocrine-spe	1108	99	3.2	814	2	JC7389	thyroid stimulat
1036	100	3.2	881	2	T01269	serine/threonine-s	1109	99	3.2	860	2	C86203	hypothetical prote
1037	100	3.2	1109	2	C84545	probable disease r	1110	99	3.2	940	2	H86420	probable receptor-
1038	100	3.2	1161	2	T45294	hypothetical prote	1111	99	3.2	963	2	T19140	hypothetical prote
1039	100	3.2	1182	2	I48378	hairless protein -	1112	99	3.2	1000	2	C82630	serine proteinase
1040	100	3.2	1240	2	T06404	resistance complex	1113	99	3.2	1097	2	T49187	hypothetical prote
1041	100	3.2	1420	2	T37781	probable cytoskele	1114	99	3.2	1147	2	T42627	ADP-ribosylation f
1042	100	3.2	1687	2	T30176	EGF repeat transme	1115	99	3.2	1217	2	T52348	disease resistance
1043	100	3.2	1791	2	T02345	hypothetical prote	1116	99	3.2	1317	2	T03748	apoptosis associat
1044	100	3.2	1802	2	T00020	bacterial blight-r	1117	99	3.2	1405	2	T04426	hypothetical prote
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-	1118	99	3.2	1532	2	A61262	collagen alpha 1(X
1046	100	3.2	2459	2	AF2136	peptide synthetase	1119	99	3.2	1538	2	E70874	probable ppsB prot
1047	99.5	3.2	108	2	S08315	cell wall protein	1120	99	3.2	1694	2	S50065	sialoadhesin - mou
1048	99.5	3.2	177	2	T07642	PEARL1 protein h	1121	99	3.2	1799	1	S44920	ZK688.5 protein -
1049	99.5	3.2	230	2	A44074	probable EGF-like	1122	99	3.2	2029	1	TDFFLK	protein-tyrosine-p
1050	99.5	3.2	280	2	I48713	Phox2 homeodomain	1123	99	3.2	2088	2	E71436	hypothetical prote
1051	99.5	3.2	293	2	C75421	hypothetical prote	1124	99	3.2	6420	2	T30283	polyketide synthas

1125	98.5	3.1	230	2	T22763	hypothetical prote	1198	97.5	3.1	352	2	S22395	fetuin precursor -
1126	98.5	3.1	254	2	D88560	protein F58A4.1 [l	1199	97.5	3.1	429	2	UC4965	elki protein - mou
1127	98.5	3.1	322	2	I17461	proteinizing hormon	1200	97.5	3.1	460	2	T23087	hypothetical prote
1128	98.5	3.1	349	2	T15422	hypothetical prote	1201	97.5	3.1	464	2	S22697	extensin - Volvox
1129	98.5	3.1	379	2	S50125	larval glue protei	1202	97.5	3.1	497	2	F83634	hypothetical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	hypothetical prote
1131	98.5	3.1	393	2	S62335	I71-7 protein - fr	1204	97.5	3.1	521	2	S54266	alpi2 protein - fi
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	glycoprotein gc -
1133	98.5	3.1	464	2	D72653	hypothetical prote	1206	97.5	3.1	563	2	A75594	lysine decarboxy
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	ferredoxin-nitrite
1135	98.5	3.1	514	2	A44100	cell adhesion mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypothetical prote
1137	98.5	3.1	700	2	I77463	luteinizing hormon	1210	97.5	3.1	626	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	UC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	PTB-associated spl	1212	97.5	3.1	627	1	AB0535	hypothetical prote
1140	98.5	3.1	770	2	T22808	hypothetical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhoGAP protein [lm	1214	97.5	3.1	662	2	A40228	neurexin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDBE23	immediate-early pr
1143	98.5	3.1	862	2	E88594	protein Y48A6.11	1216	97.5	3.1	710	2	D96728	hypothetical prote
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	Ompa family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypothetical prote
1146	98.5	3.1	947	2	T26314	hypothetical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verpoin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypothetical prote	1222	97.5	3.1	832	2	H96651	protein T3P18.19 l
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	A54809	disease resistance
1151	98.5	3.1	1396	2	A44453	translacion initia	1224	97.5	3.1	921	2	AE0332	conserved hypochet
1152	98.5	3.1	1774	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypothetical prote
1153	98.5	3.1	2180	2	T29764	hypothetical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypothetical prote
1155	98	3.1	182	2	T07641	pEARL1 protein h	1228	97.5	3.1	1258	2	UC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1158	98	3.1	303	2	S40973	hypothetical prote	1231	97.5	3.1	1748	1	J01555	genome polyprotein
1159	98	3.1	352	2	S09266	Ig alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypothetical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	238	2	T26419	hypothetical prote
1162	98	3.1	499	2	A12449	hypothetical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	B26683	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A39364	GDP-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypochet
1166	98	3.1	538	2	A70836	PRR2 delta - human	1239	97	3.1	395	2	AB6166	protein F2187.6 [l
1167	98	3.1	553	1	A42499	hypothetical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	560	1	WPH1M	mullerian inhibiti	1241	97	3.1	400	1	A28172	spasmoLYsin precu
1169	98	3.1	605	2	S46940	mullerian inhibiti	1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1170	98	3.1	614	2	S27962	hypothetical prote	1243	97	3.1	428	1	TVH0EX	transforming prote
1171	98	3.1	615	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypothetical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [l	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypothetical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlpd -	1247	97	3.1	500	2	D97302	hypothetical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypothetical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein F40E10.4 [
1177	98	3.1	856	2	QDBEE3	HHLF1 protein - hu	1250	97	3.1	601	2	T22025	hypothetical prote
1178	98	3.1	856	2	T43631	serine/chreonine k	1251	97	3.1	632	2	T02627	hypothetical prote
1179	98	3.1	889	2	S86257	resistance to Pseu	1252	97	3.1	701	1	FOFV1R	gag polyprotein -
1180	98	3.1	896	2	S36326	clathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	UC5526	kinase-defective B	1254	97	3.1	966	2	D96662	hypothetical prote
1182	98	3.1	1216	2	T34101	hypothetical prote	1255	97	3.1	967	2	G96637	hypothetical prote
1183	98	3.1	1372	2	T25933	hypothetical prote	1256	97	3.1	1123	2	A39962	kinase-related tra
1184	98	3.1	1522	2	H88380	protein T22F7.3 [l	1257	97	3.1	1214	2	T47438	disease resistance
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	neural cell adhesi
1186	98	3.1	2115	2	S38480	nonstructural prot	1259	97	3.1	1690	2	T35694	ATP dependent DNA
1187	98	3.1	2190	2	T13828	CRSB-binding prote	1260	97	3.1	1734	2	A54602	microtubule-associ
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	hypothetical prote
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNNV2W	genome polyprotein
1190	98	3.1	3871	2	T22812	rifamycin polyketi	1263	97	3.1	3034	2	T14119	seven-pass transme
1191	98	3.1	5069	2	T17464	probable arabinosa	1264	96.5	3.1	346	2	S19129	proline-rich prote
1192	97.5	3.1	215	2	S55925	insulin-like growt	1265	96.5	3.1	350	2	E75341	peptidyl-prolyl ci
1193	97.5	3.1	266	1	A35037	transcription coac	1266	96.5	3.1	419	2	G70602	hypothetical prote
1194	97.5	3.1	268	2	S71830	interferon respons	1267	96.5	3.1	430	2	I48755	msADPa - mouse
1195	97.5	3.1	306	2	A46241	extensin-like prot	1268	96.5	3.1	444	2	B36389	transcription fact
1196	97.5	3.1	306	2	T09067	transforming prote	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TWMSFB		1270	96.5	3.1	487	2	F70765	hypothetical prote

1271	96.5	3.1	514	2	A31643	cell adhesion 80K	1344	95.5	3.0	1159	2	I38465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypother	1345	95.5	3.0	1255	2	T31065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipaH protein - Shi	1346	95.5	3.0	1256	2	T31066	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastric
1275	96.5	3.1	635	2	F70874	probable membrane	1348	95.5	3.0	1630	2	T00390	KIAA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	I38408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	796	2	E96654	hypothetical prote	1353	95	3.0	239	2	S25618	hypothetical prote
1281	96.5	3.1	825	1	EDBEXD	immediate-early pr	1354	95	3.0	241	2	D43733	heretulin precursor
1282	96.5	3.1	1021	2	A86421	Receptor-like seri	1355	95	3.0	273	2	C70551	hypothetical prote
1283	96.5	3.1	1209	2	T00373	hypothetical prote	1356	95	3.0	326	2	A59232	ABA-responsive pro
1284	96.5	3.1	1241	2	T18311	hypothetical prote	1357	95	3.0	338	2	T06336	proline-rich prote
1285	96.5	3.1	1557	2	T02859	probable serine/th	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	2282	2	T42717	DNA-binding protei	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2352	2	T30201	Notch homolog prot	1360	95	3.0	477	2	S53362	mucin 5AC (clone J
1288	96.5	3.1	26926	1	I38344	titin, cardiac mus	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96	3.1	214	2	T10737	extensin-like cell	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	240	2	A24264	proline-rich prote	1363	95	3.0	636	2	I61718	neu differentiation
1291	96	3.1	287	2	C75494	cell division prot	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	346	2	JA0159	cysteine proteinas	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	445	2	T05987	hypothetical prote	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	451	2	D88395	hypothetical prote	1367	95	3.0	673	2	T48012	hypothetical prote
1295	96	3.1	483	2	S12741	protein_F53A3.6 [i	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	537	1	F0MWGV	transcription fact	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	580	2	T43481	gag polyprotein -	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	594	2	S33561	probable mucin DKF	1371	95	3.0	776	2	C96554	unknown protein [i
1299	96	3.1	598	2	T48822	ref(2)P protein -	1372	95	3.0	799	2	T48889	serine/threonine p
1300	96	3.1	635	1	WMBSW6	hypothetical prote	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	858	1	IJRTNC	capsid protein - n	1374	95	3.0	891	2	G84693	phosphoprotein, s
1302	96	3.1	883	2	A96662	neural cell adhesi	1375	95	3.0	901	2	A44825	probable proline-r
1303	96	3.1	907	2	A22951	hypothetical prote	1376	95	3.0	903	2	S60257	phosphoprotein, s
1304	96	3.1	910	2	H98331	cell division prot	1377	95	3.0	943	2	T34847	meltrin alpha - mo
1305	96	3.1	969	2	A75634	cell division prot	1378	95	3.0	1024	2	S18251	probable transcrip
1306	96	3.1	1216	2	T26104	McrB-related prote	1379	95	3.0	1209	2	T13153	collagen alpha 1(X
1307	96	3.1	1231	2	S30185	hypothetical prote	1380	95	3.0	1324	2	T14070	branna associated
1308	96	3.1	1544	2	E94931	insulin receptor s	1381	95	3.0	1474	2	B85188	peptide synthetase
1309	96	3.1	1615	2	B49502	phosphoinositide-b	1382	95	3.0	1616	2	G70668	retrotransposon li
1310	96	3.1	1737	2	T00209	protein-tyrosine-p	1383	95	3.0	1731	2	AB3045	polyketide synthas
1311	96	3.1	1767	2	A49502	MEGF8 protein - hu	1384	95	3.0	1731	2	B98241	ice nucleation pro
1312	96	3.1	1844	1	RRWETM	protein-tyrosine-p	1385	95	3.0	1770	2	T18551	hypothetical prote
1313	96	3.1	2529	2	A56923	genome polyprotein	1386	95	3.0	1806	1	CGHUIE	saframycin Mxi syn
1314	96	3.1	5376	2	T42215	transcription fact	1387	95	3.0	2090	2	T30075	collagen alpha 1(X
1315	95.5	3.0	188	2	D29149	zonadhesin - mouse	1388	95	3.0	2148	2	A56011	hypothetical prote
1316	95.5	3.0	284	2	F95320	proline-rich prote	1389	95	3.0	2274	2	T30258	transcription fact
1317	95.5	3.0	366	1	TDMSM4	conserved hypother	1390	95	3.0	3084	1	MMMSA	adenomatous poly
1318	95.5	3.0	382	2	S75823	monocyte surface g	1391	94.5	3.0	3084	1	MMMSA	laminin alpha-1 ch
1319	95.5	3.0	384	2	S51796	threonine synthase	1392	94.5	3.0	211	2	T03381	high sulfur zein p
1320	95.5	3.0	435	2	T46443	vasodilator-stimul	1393	94.5	3.0	255	2	B75309	hypothetical prote
1321	95.5	3.0	451	2	S71754	hypothetical prote	1394	94.5	3.0	255	2	S31096	proline-rich prote
1322	95.5	3.0	479	2	D70676	cellular hepatitis	1395	94.5	3.0	270	2	B87649	hypothetical prote
1323	95.5	3.0	486	2	AB2375	probable PE protei	1396	94.5	3.0	277	2	I38857	microtubule-associ
1324	95.5	3.0	486	2	A98308	succinate semialde	1397	94.5	3.0	298	2	H87533	peptidase, M23/M37
1325	95.5	3.0	501	2	S76563	attK protein (U594	1398	94.5	3.0	301	2	D87684	transcription regu
1326	95.5	3.0	507	1	A46713	hypothetical prote	1399	94.5	3.0	358	2	A61188	probable transcrip
1327	95.5	3.0	553	2	C75318	erythropoietin rec	1400	94.5	3.0	376	2	H82988	hypothetical prote
1328	95.5	3.0	570	2	A48836	hypothetical prote	1401	94.5	3.0	393	2	B82283	conserved hypother
1329	95.5	3.0	571	2	T43456	fibropellin C prec	1402	94.5	3.0	464	2	A83557	probable amidease p
1330	95.5	3.0	573	2	B70726	hypothetical prote	1403	94.5	3.0	569	2	T19128	hypothetical prote
1331	95.5	3.0	624	2	T49366	probable secB - My	1404	94.5	3.0	630	2	A39344	tumor-associated m
1332	95.5	3.0	630	2	T31798	myocyte-specific e	1405	94.5	3.0	665	2	E75461	probable cell wall
1333	95.5	3.0	650	2	S44806	hypothetical prote	1406	94.5	3.0	708	2	JC4364	gelatinase B (EC 3
1334	95.5	3.0	685	2	C56591	Flt09.6 protein -	1407	94.5	3.0	719	2	T33170	hypothetical prote
1335	95.5	3.0	710	1	S70965	E75 B steroid rece	1408	94.5	3.0	860	2	I48839	tenascin-X - mouse
1336	95.5	3.0	722	2	T22359	serine/threonine-s	1409	94.5	3.0	921	2	S42617	collagen alpha 1(I
1337	95.5	3.0	740	2	B87599	hypothetical prote	1410	94.5	3.0	985	2	T06049	hypothetical prote
1338	95.5	3.0	790	1	TVHUTT	hypothetical prote	1411	94.5	3.0	1006	2	T00050	hypothetical prote
1339	95.5	3.0	880	2	D89756	nerve growth facto	1412	94.5	3.0	1092	1	JN0635	neural cell adhesi
1340	95.5	3.0	943	2	E84429	protein_T23E7.2b l	1413	94.5	3.0	1191	2	T13850	gene u-shaped prot
1341	95.5	3.0	987	2	A54092	probable receptor-	1414	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1342	95.5	3.0	1027	2	I38759	protein-tyrosine k	1415	94.5	3.0	1690	1	CGHUIB	collagen alpha 4(I
1343	95.5	3.0	1054	2	A30239	zinc finger/leucina	1416	94.5	3.0	2062	2	G96602	probable receptor
						hydroxymethylgluta				2302	2	T14328	protein-tyrosine-p

1417	94.5	3.0	2386	1	PMH1	fibronectin precu
1418	94.5	3.0	2484	2	T26216	hypothetical prote
1419	94.5	3.0	2607	2	T26215	hypothetical prote
1420	94	3.0	157	2	T02034	early light-induce
1421	94	3.0	263	2	S57346	interleukin-15 rec
1422	94	3.0	277	2	E72564	hypothetical prote
1423	94	3.0	293	2	T22919	hypothetical prote
1424	94	3.0	329	2	T10064	cytokinin-induced
1425	94	3.0	338	2	S28004	probable cell surf
1426	94	3.0	346	2	S76923	hypothetical prote
1427	94	3.0	356	2	A96826	T8K1.4.10 [imported
1428	94	3.0	421	2	T38309	probable cell wall
1429	94	3.0	456	2	A40492	early growth respo
1430	94	3.0	466	2	A46389	transcription fact
1431	94	3.0	476	2	B44997	merozoite surface
1432	94	3.0	522	2	S41819	nucleoporin p62 -
1433	94	3.0	559	2	C75286	hypothetical prote
1434	94	3.0	590	2	B36789	hypothetical prote
1435	94	3.0	639	2	I61719	neu differentiation
1436	94	3.0	648	2	S50856	whn protein - rat
1437	94	3.0	677	2	UC7303	peccate lyase (EC
1438	94	3.0	693	1	A41090	serine/threonine s
1439	94	3.0	791	2	S67265	hypothetical prote
1440	94	3.0	811	2	T36581	probable transmem
1441	94	3.0	862	2	S51493	major nitroge reg
1442	94	3.0	865	1	D70986	probable ABC trans
1443	94	3.0	878	1	A40091	interleukin-3 rece
1444	94	3.0	898	2	A40114	fasciclin II precu
1445	94	3.0	918	2	UC4361	scavenger receptor
1446	94	3.0	927	2	A46085	transcription fact
1447	94	3.0	939	2	C70876	hypothetical prote
1448	94	3.0	979	2	A70848	probable membrane
1449	94	3.0	1007	2	G96606	disease resistance
1450	94	3.0	1137	2	G70868	probable regulator
1451	94	3.0	1236	2	E70977	hypothetical prote
1452	94	3.0	1320	2	UC5630	TCOP1 protein - mo
1453	94	3.0	1331	2	A48954	mannan endo-1,4-b
1454	94	3.0	1335	2	T18289	racGAP protein - s
1455	94	3.0	1429	2	T13720	gene expanded prot
1456	94	3.0	1549	2	T11974	glutamate synthase
1457	94	3.0	1560	2	T00080	hypothetical prote
1458	94	3.0	2153	2	T30074	hypothetical prote
1459	93.5	3.0	172	2	D41132	collagen-related p
1460	93.5	3.0	278	2	T27610	hypothetical prote
1461	93.5	3.0	299	2	G70784	probable mmp3 pro
1462	93.5	3.0	305	2	T46721	hypothetical prote
1463	93.5	3.0	352	2	T06482	probable cell wall
1464	93.5	3.0	362	2	S61924	cyst wall protein
1465	93.5	3.0	391	2	I50702	transcription fac
1466	93.5	3.0	458	2	B87335	hypothetical prote
1467	93.5	3.0	461	1	A35356	tumor necrosis fac
1468	93.5	3.0	490	2	AG1107	internalin G [limp
1469	93.5	3.0	522	2	T36501	probable serine/th
1470	93.5	3.0	530	2	A53437	poliovirus recepto
1471	93.5	3.0	556	2	T42100	serine/threonine p
1472	93.5	3.0	577	2	T18116	hypothetical prote
1473	93.5	3.0	662	2	T46005	receptor-like prot
1474	93.5	3.0	691	2	B75622	hypothetical prote
1475	93.5	3.0	718	2	T05840	subtilisin-like pr
1476	93.5	3.0	719	2	F96577	hypothetical prote
1477	93.5	3.0	854	2	A96574	protein F12M16.30
1478	93.5	3.0	909	1	ORX112	LDL receptor 2 pre
1479	93.5	3.0	919	2	F83257	hypothetical prote
1480	93.5	3.0	998	2	T35745	probable ATP-bind
1481	93.5	3.0	1121	2	UC7329	WD-repeat protein
1482	93.5	3.0	2109	2	E89066	protein H05009.1 [
1483	93.5	3.0	2150	2	T33247	hypothetical prote
1484	93.5	3.0	2295	2	C86369	protein unc-52 [lm
1485	93.5	3.0	3375	2	T19821	hypothetical prote
1486	93	3.0	209	2	T02262	high-methionine d-
1487	93	3.0	221	2	T07079	leucine-rich repea
1488	93	3.0	235	2	PC2022	mucin like protein

1490	93	3.0	338	2	S01359	salivary glue prot
1491	93	3.0	338	2	S38030	suppressor protein
1492	93	3.0	384	2	H70580	hypothetical prote
1493	93	3.0	413	2	AH2743	conserved hypotet
1494	93	3.0	416	2	G97524	hypothetical prote
1495	93	3.0	438	2	G87675	arylesterase-relat
1496	93	3.0	453	2	B42093	serum response fac
1497	93	3.0	455	2	B82515	alpha-L-fucosidase
1498	93	3.0	558	2	T50742	protoporphyrin IX
1499	93	3.0	560	1	JC4795	plasma hyaluronan
1500	93	3.0	586	2	H86914	conserved hypotet

## ALIGNMENTS

RESULT 1  
 Insulin-like growth factor acid-labile chain - baboon  
 C/Species: Papio sp. (baboon)  
 C/Date: 17-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-May-1997  
 C/Accession: JC5239  
 R:Delhanty, P.; Baxter, R.C.  
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996  
 A/Title: The Cloning and expression of the baboon acid-labile subunit of the insulin-like  
 A/Reference number: JC5239; MUID:97040714; PMID:8886027  
 A/Contents: liver  
 A/Accession: JC5239  
 A/Molecule type: mRNA  
 A/Residues: 1-605 <DBL>  
 A/Cross-references: UNIPARC:UPI000000D50E  
 C/Comment: This factor is structurally related to proinsulin and have insulin-like metal

Query Match 10.3%; Score 322; DB 2; Length 605;  
 Best Local Similarity 36.2%; Pred. No. 2e-11;  
 Matches 100; Conservative 39; Mismatches 97; Indels 40; Gaps 11;

Qy	7	ILPLLL-LALG-----PGVQ-----CPSCQCSOPQ-----TVFCTAROGTT	45
Db	8	LALALLLSVNALGPRSLBGAERGTPGEABGPACPAACSYDENVNELSVFCSSRLTR	67
Qy	46	VPRDVPDVTGLVYFENGITMDASSPAGLPGQLDLSONQIASRLPRLLL-----	98
Db	68	LPGIGPGTQALWLDNSNLSSIPPAPFRNLSSIAFLNLQGGQLGSLE--PQALGLENLCH	126
Qy	99	LDLSHNSILAEFGIIDTANVENLRAGLG--LQQLDELFPSRLNTHLDVSDQTER	155
Db	127	LHLERNQLRSIAVGTF--ATTPALALIGSNRLSRLEDELFEGLNTWDLNIGWNSLAV	184
Qy	156	VP-FVIRGRLGRLRLAGNTRIAQLRPEDLAGALQEDVSNLSIQALPGDLSGLFPR	214
Db	185	LPPAARFGAGLRELVLAGN-RLAYIQPALFSGLAIRELDLSRNALRAKANVFAQLPR	243
Qy	215	LRLLAARNPFCVCPCLSWFG---PWVRESHTLA	246
Db	244	LQKLIVDRMLIAAVAPGAFGLKALRWLDLSHRVA	279

RESULT 2  
 A41915  
 Insulin-like growth factor-binding complex acid-labile chain precursor - human  
 N/Alternate names: Acid-labile Subunit (ALS)  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C/Accession: A41915  
 R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.  
 Mol. Endocrinol. 6, 870-876, 1992  
 A/Title: Structure and functional expression of the acid-labile subunit of the insulin-1  
 A/Reference number: A41915; MUID:92357025; PMID:1379671  
 A/Accession: A41915  
 A/Status: preliminary  
 A/Molecule type: mRNA; protein  
 A/Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:  
A;Experimental source: liver  
F;75-92/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>  
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>  
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 9.6%; Score 302; DB 2; Length 605;  
Best Local Similarity 35.5%; Pred. No. 2.9e-10;  
Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

QY 7 LLLPLLLL-LALG-----PGVG-----CPSGCQSQPQ-----TVFCTAROGTT 45  
DB 8 LALLALLLSWVAGPRLSEAGDPTGTEAGPACVCSYDDADSLVFCSSRLTR 67  
QY 46 VPRDVPDVTGVVFNFGITMLDASSFAGLPGLQLDLSONQASLRPLRL 98  
DB 68 LPDGVPGTQALWDGNNLSSVPPAFQNLSSGLFNLQGLQGLSLR-PQALLGLENLCH 126  
QY 99 LDLSHNSLLALEPGLIDTANVEALRLAGLG---LQQLDEGLFSLRLNHLDVDSDNOLER 155  
DB 127 LHLERNQLRSALGTF--AHTPALASLGLSNNLSRLSDGLFEGLSGLDNLGNLSLAV 184  
QY 156 VP-FVIRGLRGLTRLAGNTRIAQLRPEDLAGLAQLDLVDVNSLQALPGDLSGLFPR 214  
DB 185 LPDAAPFGLSGSLRELVLGN--RLAYLQPALFSGLAELRDLDSRLAALRAIKANVFQPLR 243  
QY 215 LRLLAARNPFNCVCLSNFG----PMVRESHTLA 246  
DB 244 LQKLYLRNLIAAVAGFLGLKALRWLDLSHRVA 279

RESULT 3  
NBHUIA  
platelet glycoprotein Ib alpha chain precursor - human  
N;Alternate names: membrane glycoprotein Ib alpha chain  
N;Contains: glycosalican  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence, revision 28-Dec-1987 #text change 09-Jul-2004  
C;Accession: A94174; S16945; I55355; A27075; A27102  
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987  
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p  
A;Reference number: A94174; MUID:87289655; PMID:3303030  
A;Accession: A94174  
A;Molecule type: mRNA  
A;Residues: 1-626 <LQ>  
A;Cross-references: UNIPROT:P07359; UNIPARC:UPI0000012B962; GB:J02940; NID:g183499; PIDN:  
R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J.  
Thromb. Haemost. 61, 448-453, 1989  
d;Cloning of a GPIb and characterization of human blood platelet mRNA and construction of  
A;Reference number: A60435; MUID:90020160; PMID:2799758  
A;Accession: A60435  
A;Molecule type: mRNA  
A;Residues: 207-467 <WIC>  
A;Cross-references: UNIPARC:UPI00000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987  
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem  
A;Reference number: A94173; MUID:87289654; PMID:3497398  
A;Accession: A94173  
A;Molecule type: protein  
A;Residues: 17-315 <FII>  
A;Cross-references: UNIPARC:UPI00000174312  
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.  
Eur. J. Biochem. 199, 389-393, 1991  
A;Title: Identification of the disulphide bonds in human platelet glycosalican.  
A;Reference number: S16945; MUID:91301149; PMID:2070794  
A;Accession: S16945  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 224-227;262-270;277-282 <HES>  
A;Cross-references: UNIPARC:UPI00000174313; UNIPARC:UPI00000174314; UNIPARC:UPI00000174315  
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.  
J. Biol. Chem. 267, 10055-10061, 1992  
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t  
ations.  
A;Reference number: I55355; MUID:92250564; PMID:1577776  
A;Accession: I55355  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 412-427 <RES>  
A;Cross-references: UNIPARC:UPI0000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:  
A;Note: variant D  
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates  
C;Comment: Platelet activation apparently involves disruption of the macromolecular comp  
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un  
C;Comment: Glycosalican, which is approximately coextensive with the extracellular part  
C;Genetics:  
A;Gene: GDB:GPIBA; GPIB  
A;Gene-references: GDB:I18806; OMIM:231200  
A;Map position: 17pter-17p12  
C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)  
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein re  
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem rep  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>  
F;48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;379-430/Region: proline/threonine-rich 9-residue repeats  
F;502-540/Domain: transmembrane #status predicted <TRM>  
F;541-626/Domain: intracellular #status predicted <INT>  
F;37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 9.0%; Score 282; DB 1; Length 626;  
Best Local Similarity 24.0%; Pred. No. 4.4e-09;  
Matches 160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;

QY 9 LPLLLLLALGFGVCGSGCQSQPQ---VFCTAROGTTVPRDVPDVTGVVFN--- 62  
DB 1 MPELLLLLPLSPHPPHPICEVSKVASHLEVNCNRLTALPPDLPKDTTILHSENILY 60  
QY 63 -----GITWLDASSF-----AGLPGQLDLSONQIASI-----RLPRLLL 98  
DB 61 TFSLATMYPYRLTQLNLDRCCELTKLQVDTPLVIGTLDLSHNLQSLPLGLQTPALUTV 120  
QY 99 LDLSHNSLLALEPGLI-DTANVEALRLAGLQQLDEGLFSLRLNHLDVDSDNOLERVP 157  
DB 121 LDVSNRLTSPLGALRGELQELYLKGNELKTLPGCLLTPTPKLEKLSLANNLTLP 180  
QY 158 P-VIRGLRGLTRLAGNTRIAQLRPEDLAGLAALQELVDVNSLQALPGDLSG--LPRP 214  
DB 181 AGLLENLDTLLQEN-----SLYTPKPGFGSHLLPF 215

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OY 215 LRLAARNPENCVCPLSMFGWRES-----HTLASPEETRC----- 253
D 216 AFLHG---NPMWLCNCEILYFRRMLODNANVYVWKGQVDVKAMTSNVA5QCDNSDKFPV 272
OY 254 -HPPKNAGRILILE--LDVADFGCPATTTATVPTTRPVVREP-----TA 295
D 273 YKYPKGCPTLQDEBDTLDYDYYPEEDTSGDKVRAIRIVVKKPPTKATTPWGLFTYSWSTA 332
OY 296 LSSSIAPTWLSPTAPATE-----ASPSPTAPPVGV---PQ 330
D 333 SLDSQMPSSLHPTQSTYKQTTPRPWTNFTLHMSITFSKTPKSTTEPTSPPTSEV 392
OY 331 PDCPSPTCLNGCTGHLGTRHILACLCPGFTGLYCESQMGQSTRSPPTVTPRPSLT 390
D 393 PEPANMTTLEPTP-----SPTTP-----PTSEPA5PPTPEPTPIPT 431
OY 391 LGIEP---VSPTSILAVGLORYIQGSS--VOLRSILRTYNNLSGPDRLVTLR--LPASILA 443
D 432 IATSEPTILVSATSLITPKSTFLTTKPVSLLESTKTKTIPELDQPPRLRGVLQGLHSSRN 491
OY 444 EYTVQLRPNATYSVCVMPPLG-----PGRV-PEGGEACGEAHT 480
D 492 D---PFLHPD---FCCILPLGFEYVGLFWMLPASVLLILLSWGVHKPQALDSGGAL 545
OY 481 PPAVSHNAPVTQAREGNLP---LLI---APALAVALLAALAAVGAAYCVRGRAMAA 533
D 546 TTAQTGTHLELRGQGVTPRAMLFLRGSLLPTFRSSLLFWVRPNRGVPLVAGRPSAL 605
OY 534 AODKQO 539
D 606 SQGRGO 611

```

## RESULT 4

```

JCI1282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI1282
R:Daiz, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A:Reference number: JCI1282; MUID:93038676; PMID:1384485
A:Accession: JCI1282
A:Molecule type: mRNA
A:Residues: 1-603 <DAL>
A:Cross-references: UNIPROT:P35859; UNIPARC:UPI0000125918; GB:S46785; NID:g258002; PIDN:
A:Experimental source: liver
A:Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

```

```

Query Match 9.0%; Score 281.5; DB 2; Length 603;
Best Local Similarity 32.4%; Pred. No. 4.5e-09;
Matches 92; Conservative 49; Mismatches 106; Indels 37; Gaps 11;

OY 6 PLLPLLL-LALGP-GVGG-----CPSGCCOSQPO-----TVCTARQGT 45
D 8 PALVLLAFWVALGCHLQGTDPGASADAEGPCPVACTCSHDDYDELVSFCSSRLTH 67
OY 46 VPRDVPDPTVGIVFENGITMLDASSFAGLPGQLDLDSQNIASLR-----LPLLLL 99
D 68 LPDDIPVSTRALMDGNLSSISPSAFAFONLSSLDPLNLSQSWLRSLPEALGLQNLYYL 127
OY 100 DLNHSILALBPGIL-DTANVEALRLAGLQQLDGLFSRLRNHLDLVDSDNQLRRVP- 157
D 128 HLERNRLNLAAGLTPHTPSLASLSLSNULGRLEGLFGQSHLMDLWGNLSLVLPD 187
OY 158 PVIRGLRGITRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLOALPDLGLFPRLR 217
D 188 TVFGQLGNLHVLVAGN-KLTVLQPALFGQLGELRLDLDSRNALRSVKANVFHLPRLQK 246

```

```

OY 218 LLAARNPENCVCPLSMFG---PMVRESHTLAS-PEETCHRP 256
D 247 LYLDRLNLITAVAPAGAFGLKMKALRLMDLSHNRVAGLMEDT---FP 287

```

## RESULT 5

```

JCI6128
Insulin-like growth factor binding complex acid labile chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JCI6128
R:Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A:Title: Organization and chromosomal localization of the gene encoding the mouse acid l
A:Reference number: JCI6128; MUID:96413591; PMID:8816745
A:Accession: JCI6128
A:Molecule type: DNA
A:Residues: 1-603 <BOI>
A:Cross-references: UNIPROT:P70389; UNIPARC:UPI0000000891; GB:U66900; NID:g1621612; PIDN:
C:Comment: This protein is a serum protein and it is of the ternary complex in the physio
A:Gene: als
A:Map position: 17

```

```

Query Match 8.9%; Score 278.5; DB 2; Length 603;
Best Local Similarity 32.8%; Pred. No. 6.7e-09;
Matches 90; Conservative 48; Mismatches 101; Indels 35; Gaps 10;

```

```

OY 6 PLLPLLL-LALGP-GVGG-----CPSGCCOSQPO-----TVCTARQGT 45
D 8 PALVLLAFWVALGCHLQGTDPGASADAEGPCPVCTCSYDDYDELVSFCSSRLTHQ 67
OY 46 VPRDVPDPTVGIVFENGITMLDASSFAGLPGQLDLDSQNIASLRPLLL----- 98
D 68 LPDGIPTVSTRALMDGNLSSISPSAFAFONLSSLDPLNLSQSWLRSLPEALGLQNL 126
OY 99 LDIHSNLSLALBPGIL-DTANVEALRLAGLQQLDGLFSRLRNHLDLVDSDNQLRRVP 157
D 127 LHERNLRLSLAAGLFRHPSPSLASLSGNLQLRLEEGFLRGSLHMDLWGNLSLVLP 186
OY 158 -PVIRGLRGITRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLOALPDLGLFPRLR 216
D 187 DTFVQGLGNLHVLVAGN-KLTVLQPALFGQLGELRLDLDSRNALRSVKANVFHLPRLQ 245
OY 217 LLAARNPENCVCPLSMFG---PMVRESHTLAS 246
D 246 KLYLDRLNLITAVAPRAFLGKALKRLMDLSHNRVA 279

```

## RESULT 6

```

T42218
Slit-1 protein homolog - rat
N:Alternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42218
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: T4126; MUID:98360089; PMID:9693030
A:Accession: T42218
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NAK>
A:Cross-references: UNIPROT:O88279; UNIPARC:UPI000004F20B; EMBL:AB011530; NID:g3449289; I
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF4
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re
Query Match 8.9%; Score 278; DB 2; Length 1531;
Best Local Similarity 25.8%; Pred. No. 2.1e-08;

```



```
Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;
Qy 6 PLLPLLLLALGPGVQCPCSCQSPQTVCTARQGTTPRDPVDPDTVGLYVFENGIT 65
Db 16 PELWLLWAAARUGATACPALCTCT-GTTVDCHGTGLQAI-PKNIPRTERLELNGNIT 74
Qy 66 MLDASSFAGLPGLQLLDLSQNOIASLRPLRLLLDLSHNSLLALEPGIL-DTANVEALRL 124
Db 75 RIHKNDFAGLKQLRVLMENQIG-----AVERGAFDDMKELERLRL 116
Qy 125 AGLGLOQDDEGLFSLRNHLHDLDVSDNOLERP-VPIRGLRGLTRLRAGNTRIAQLRPE 183
Db 117 NRNOLOVLPELLFQNNQALSRDLDSLSLQAVPKAFRGATDLKNLQLDKN-QISCIERG 175
Qy 184 DLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPNCVPLSWFGPWVRESHV 243
Db 176 AFRALRGLLEVITLNNNITITPVSSFNHMPKLTFLHSHNLFCDCHLAWLSQWLQ-RP 234
Qy 244 TLASPEETRCHPPPKNAGRLLELYADFGCPATTTTATVTPTRPVVREPTALSSLAFT 303
Db 235 TIGL--FTQCGPASLRGLNVAEVQKSEFSCSQGGAQVPA-----CTLSSGSCPA 284
Qy 304 WLSPTAPATEAPSPSTAPTPVGPVPOQ-----DCPSTCLNGTCHLG----- 348
Db 285 MCSCSNGIVDCRGKGLTAIPANLPETMTAIRLELNGIKSIPP-----GAFSPYR 333
Qy 349 -----FRHLACLCPGSGFTGLYCESQMGQTRPSPTVTPRPPRSLTGLIEPV--PT 399
Db 334 KLRRIDLSNNOIAETAPAFQGL-----RSLNSLVLYGNKTTDLPR 374
Qy 400 SLRVGLQRYLOGSSVQLRSRLTYRNLSGFD--KRLVTLRLPA-----SLAEYVTVOL 450
Db 375 GVFGGLY-----TLQALLNANKINCIREDAFQDLQNLSLSLYDNKIQSLAKGFTTSL 428
Qy 451 RPNATYSVCVMP 462
Db 429 RAIOTLHLAQN 440

RESULT 7
A53531
oncofetal trophoblast glycoprotein 5T4 precursor - human
N;Alternate names: oncofetal antigen 5T4
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A53531; S40087
R;Myers, K.A.; Rahn-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.
J. Biol. Chem. 269, 9319-9324, 1994
A;Title: Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen
A;Reference number: A53531; MUID:94179356; PMID:8132670
A;Accession: A53531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-420 <MEY>
A;Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:Z29083; NID:G435654; PID
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted <MAT>

Query Match 8.4%; Score 264.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 2.9e-08;
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;

Qy 2 CSVRP-----LLPLLLLALG-----RGVGGCRS 26
Db 5 CSRGPAGDGRRLRLARLALVLLGWSSSSPTSSASSFSAPPFLASAVSAQPLPDQCPA 64
Qy 27 GCQCSQ-PQTVCTARQGTTPRDPVDPDTVGLYVFENGITMLDASSFAGLP---GLQLLD 82
Db 65 LCECSEARTKVCVRNLTVEPTDLPAYVVRNLTGNQLAVLPAGAFARRPPLAELAA 124
Qy 83 LSQNOIASLR-----LPRLLLDLSHNSLLALEPGILDNTANVEALRLAGLGLQQLDEGL 136
```

```
Db 125 LGSRLDEVACAFELPSLRQLDLSHNPLADLSPFAFGSNASV-----SAPSPL 175
Qy 137 FSLRLNLHDLDVSDNQLER-----VPPVI--RGLRGLTRLRAGNTRIAQLRPEDLAGL 188
Db 176 VELILN-HIVPPEDEQRQNSFEQMVVAALLAGRALQGLRLELASN-HFLYLPDRDVLQ 233
Qy 189 ALQELDVSNLSLQALP-----GDSGLFPRLRLAA 220
Db 234 PSRLHLDLSNNSIVSLTYVSFRNLTHLESILHLEDNALKVLHNGTLAELOGL-PHIRVF-L 291
Qy 221 ARNPFCVPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELYADFGC---PA 276
Db 292 DNNPWCCDCHMDMVTWLKETEV-VQKORLTCAYPEKMRNRVLELNSADLDCDPILPP 350
Qy 277 TTTTATV 283
Db 351 SLOTSYV 357

RESULT 8
MEGF5 protein - rat
N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13953
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
A;Cross-references: UNIPROT:O88280; UNIPARC:UPI0000005EF7A; EMBL:AB011531; NID:G3449291;
C;Gene: MEGF5
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
Query Match 8.3%; Score 261; DB 2; Length 1523;
Best Local Similarity 26.3%; Pred. No. 2e-07;
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;

Qy 24 CPSCGCSQSPQTVCTARQGTTPRDPVDPDTVGLYVFENGITMLDASSFAGLPGLQLLDL 83
Db 725 CPQCTQVE-TTVRCNRRGLHTLPKMPKDVTELYLEGNHLTAV----- 767
Qy 84 SQNOIASLRPLRLLLDLSHNSLLALEPGILDNTANVEALRLAGLGLQQLDEGLFSRLNL 143
Db 768 -PRELSTFR--QLTLIDLNSNS-----ISMLTNHTFSNMSHL 801
Qy 144 HDLDVSDNQLERP-VPIRGLRGLTRLRAGNTRIAQLRPEDLAGLALQELDVSNLSLQ 202
Db 802 STLILSYNRLRCLTPVHAFNGLSRLVLTLHGN-----DISSVPEGSFNDITLSL-- 850
Qy 203 ALPGDLSGLFPRLRLAAARNPNCVPLSWFGPWVRESHVTLASPEETRCHFPKPNAGR 262
Db 851 -----HLALGINPLHDCSLRWLSEWKAGY---KEPGIARCSSPESMADR 893
Qy 263 LLELDYADFGCPATTTTATVTPTRPVVREPTALSSSLAFTPLSPTAPATEAPSPSTAP 322
Db 894 LLITTPTHRFOCKG-----PVDINIVAKCNACLS--PCKNNGTCSQDPVEQYRCTCP 944
Qy 323 PTVGVPVPOQDC--PPSTCL-----NGGTCHLGRHH--LACLCPEGFTGLYCE 367
Db 945 YSY---KGKDKTVPINTCVQNPQCGGTCHLSHRDGFSCSPLGFEQORCE 994

RESULT 9
B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
```



C:Accession: B5665  
R:Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.  
Genes Dev. 4, 2169-2187, 1990  
A:Title: slit: an extracellular protein necessary for development of midline glia and co  
A:Reference number: A5665; MUID:19099665; PMID:2176636  
A:Accession: B5665  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1469 <ROT>  
A:Cross-references: UNIPARC:UPI0000177454; GB:X53955  
C:Genetics:  
A:Gene: FlyBase:slit  
A:Cross-references: FlyBase:FBgn0003425  
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein  
F:66-91/Domain: proteoglycan amino-terminal homology <PAH1>  
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>  
F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>  
F:221-244/Domain: proteoglycan amino-terminal homology <PA2>  
F:245-268/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>  
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F:341-364/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>  
F:365-388/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>  
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F:413-436/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>  
F:437-460/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>  
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F:485-508/Domain: proteoglycan amino-terminal homology <PA3>  
F:509-532/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
F:533-556/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F:557-580/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
F:581-604/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>  
F:605-628/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>  
F:629-652/Domain: proteoglycan carboxyl-terminal homology <PC3>  
F:653-676/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>  
F:677-700/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>  
F:701-724/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>  
F:725-748/Domain: proteoglycan carboxyl-terminal homology <PC4>  
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F:773-796/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>  
F:797-820/Domain: proteoglycan carboxyl-terminal homology <PC2>  
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F:869-892/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>  
F:893-916/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>  
F:917-940/Domain: proteoglycan carboxyl-terminal homology <PC1>  
F:941-964/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>  
F:965-988/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>  
F:989-1012/Domain: proteoglycan carboxyl-terminal homology <PC6>  
F:1013-1036/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>  
F:1037-1060/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>  
F:1061-1084/Domain: proteoglycan carboxyl-terminal homology <PC7>  
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F:1181-1204/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>  
F:1205-1228/Domain: proteoglycan carboxyl-terminal homology <PC9>  
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F:1325-1348/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>  
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F:1469-1492/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>  
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F:1709-1732/Domain: proteoglycan carboxyl-terminal homology <PC16>  
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F:1757-1780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>  
F:1781-1804/Domain: proteoglycan carboxyl-terminal homology <PC17>  
F:1805-1828/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>  
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F:1853-1876/Domain: proteoglycan carboxyl-terminal homology <PC18>  
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F:1901-1924/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR42>  
F:1925-1948/Domain: proteoglycan carboxyl-terminal homology <PC19>  
F:1949-1972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR43>  
F:1973-1996/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR44>  
F:1997-2020/Domain: proteoglycan carboxyl-terminal homology <PC20>  
F:2021-2044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR45>  
F:2045-2068/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR46>  
F:2069-2092/Domain: proteoglycan carboxyl-terminal homology <PC21>  
F:2093-2116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR47>  
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F:2237-2260/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR51>  
F:2261-2284/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR52>  
F:2285-2308/Domain: proteoglycan carboxyl-terminal homology <PC24>  
F:2309-2332/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR53>  
F:2333-2356/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR54>  
F:2357-2380/Domain: proteoglycan carboxyl-terminal homology <PC25>  
F:2381-2404/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR55>  
F:2405-2428/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR56>  
F:2429-2452/Domain: proteoglycan carboxyl-terminal homology <PC26>  
F:2453-2476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR57>  
F:2477-2500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR58>  
F:2501-2524/Domain: proteoglycan carboxyl-terminal homology <PC27>  
F:2525-2548/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR59>  
F:2549-2572/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR60>  
F:2573-2596/Domain: proteoglycan carboxyl-terminal homology <PC28>  
F:2597-2620/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR61>  
F:2621-2644/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR62>

QY	312	TEA5PSPSTAPRTGCVPRP-----	-----QCCPSTCTCNGCTGCTGTHNLACLP	DEG	360
Db	928	REYQC-----	-----LCQPGYGHKCEFMIDACYGNPCCNNMATTVLEBGRFSQC	APG	976
QY	361	FTGLYCESQM	370		
Db	977	YTGARCEINI	986		
RESULT 10					
A3665	slit protein 1 precursor - fruit fly ( <i>Drosophila melanogaster</i> )				
C:Species:	Drosophila melanogaster				
C:Date:	30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002				
C:Accession:	A3665; A31640; S13523				
R:Rotberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.					
Genes Dev.	4, 2169-2187, 1990				
A:Title:	slit: an extracellular protein necessary for development of midline glia and com				
A:Reference number:	A3665; PMID:9109965; PMID:2176636				
A:Accession:	A3665				
A:Status:	preliminary				
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A:Residues:	1-1480 <RD>				
A:Cross-references:	UNIPARC:UPI0000150F01; GB:553959; NID:g8614; PIDN:CAA37910.1; PID:g8614				
R:Rotberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.					
Cell	55, 1047-1059, 1988				
A:Title:	slit: An EGF-homologous locus of D. melanogaster involved in the development of				
A:Reference number:	A31640; PMID:8907553; PMID:3144436				
A:Accession:	A31640				
A:Molecule type:	DNA				
A:Residues:	881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA' <RO2>				
A:Cross-references:	UNIPARC:UPI000016BD7A; GB:M23543; NID:g340939; PID:g514357				
C:Genetics:					
A:Gene:	FlyBase:slit				
A:Cross-references:	FlyBase:FBgn0003425				
A:Intron:	1351/3				
C:Superfamily:	fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein repeat				
C:Keywords:	alternative splicing; growth factor				
F:66-91/Domain:	proteoglycan amino-terminal homology <PAH1>				
F:101-1124/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR1>				
F:125-146/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR2>				
F:149-172/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR3>				
F:173-196/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR4>				
F:197-220/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR5>				
F:228-272/Domain:	proteoglycan carboxyl-terminal homology <PCS1>				
F:288-313/Domain:	proteoglycan amino-terminal homology <PAH2>				
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F:767-790/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR16>				
F:791-814/Domain:	leucine-rich alpha-2-glycoprotein repeat homology <LRR17>				
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F:846-890/Domain:	proteoglycan carboxyl-terminal homology <PCS4>				
F:1028-1061/Domain:	EGF homology <EGF>				
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F:1115-1148/Domain:	EGF homology <EGF1>				
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Matches 105;	Conservative 52;	Mismatches 168;	Indels 165;	Gaps 14;	



QY 199 LSLQALPG-----DLSLFPRRLILAAARNFNCVCPISMFGPWVRES 241  
 DB 235 NSLIASVPEGLMWSLGGPNMDMRDGFDSG-----FWICDONLSIDYRWLQAO 282  
 QY 242 HTLASPEERCHFPFKNAGRLL 265  
 DB 283 KDRMFSQNDTRCAGPEAVKQOTLL 306

RESULT 13  
 A60164  
 platelet membrane glycoprotein V precursor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 12-Jan-1993 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004  
 C/Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329  
 R/Lanza, F.; Morales, M.; de la Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T.  
 J. Biol. Chem. 268, 20801-20807, 1993  
 A/Title: Cloning and characterization of the gene encoding the human platelet glycoprotein V  
 A/Reference number: A48030; NCID:94012616; PMID:8407908  
 A/Accession: A48030  
 A.Molecule type: DNA  
 A.Residues: 1-560 <LA2>  
 A/Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:9312501; PID:R.Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama, Blood 75, 2349-2356, 1990  
 A/Title: Rapid purification and characterization of human platelet glycoprotein V: the a  
 A/Reference number: A60164; NCID:90275263; PMID:2350580  
 A/Accession: A60164  
 A.Molecule type: protein  
 A.Residues: 365-384, 'X', 386-390, 'X', 392-395, 'X', 397, 188-208, 'I', 210, 27-50, 'X', 52-53, 174-  
 'XX', 108, 'T', 61-72, 'TK', 75-77, 'V', 56-57, 'G', 479-487, 'X', 489-498, 'X', 500, 'X', 502-503, 'X'  
 A/Cross-references: UNIPARC:UPI000017C2F6; UNIPARC:UPI000017C2F7; UNIPARC:UPI000017C2F8;  
 2FD; UNIPARC:UPI000017C2FE; UNIPARC:UPI000017C2FF; UNIPARC:UPI000017C300; UNIPARC:UPI000  
 R.Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.  
 Biochem. Biophys. Res. Commun. 170, 153-161, 1990  
 A/Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a  
 A/Reference number: A35483; NCID:90321220; PMID:2372284  
 A/Accession: A35483  
 A.Molecule type: protein  
 A.Residues: 145-166, 'I', 168-169, 'X', 171-172 <ROT>  
 A/Cross-references: UNIPARC:UPI000017C303  
 A/Note: this proteolytic fragment was designated peptide M392  
 A/Accession: B35483  
 A.Molecule type: protein  
 A.Residues: 121-129, 'W', 131-135, 466-468, 'X', 470 <RO2>  
 A/Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305  
 A/Note: this material was designated peptide M393 but may contain two peptides  
 A/Accession: C35483  
 A.Molecule type: protein  
 A.Residues: 252-266, 'H', 268-272, 'X', 274-279, 'I', 281-284, 'I', 286 <RO3>  
 A/Cross-references: UNIPARC:UPI000017C306  
 A/Note: this proteolytic fragment was designated peptide M401  
 R.Zafar, R.S.; Walz, D.A.  
 Thromb. Res. 53, 31-44, 1989  
 A/Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl  
 A/Reference number: A60432; NCID:89162331; PMID:2922700  
 A/Accession: A60432  
 A.Molecule type: protein  
 A.Residues: 477-478, 'FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <ZAF>  
 A/Cross-references: UNIPARC:UPI000017C307  
 R.Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993  
 A/Title: Human platelet glycoprotein V: characterization of the polypeptide and the relat  
 A/Reference number: A47507; NCID:93391348; PMID:7690959  
 A/Accession: A47507  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-560 <RBS>  
 A/Cross-references: UNIPARC:UPI000004B117; GB:I11338; NID:9388759; PIDN:AAA03069.1; PID:  
 C/Comment: This platelet membrane protein is a substrate for thrombin.  
 C/Comment: The amino end of the intact protein is blocked.  
 C/Comment: This protein is absent in Bernard-Soulier syndrome.

A/Gene: GDB:G95  
 A/Cross-references: GDB:230236; OMIM:173511  
 A/Map position: 5pter-5qter  
 C/Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prote

Query Match 7.7%; Score 240; DB 2; Length 560;  
 Best Local Similarity 27.2%; Pred. No. 1e-06;  
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QY 57 LVYFENGITWLDSSPAGLPGQLDLDSQNI-----AST--RLPRLLLDLSHNSLALAE 110  
 DB 127 LPLDHAARKGIDDMQKLVNLOELANQQLDPLFASLFTNLENLKLDDLSONLTHLP 186  
 QY 111 PGILDT-ANVEALRLAGLQQLDEGL-----FSRLRNLD 145  
 DB 187 KGLLGAQAKERLLLSNRNLSVDSGLNSLGLATLQFHRNHRISAPGAFRLPNLSS 246  
 QY 146 LDVS-----DNQLEVPVPIRG----- 162  
 DB 247 LTLSRNHLAFLPSALFLASHNLTLLTFENPLAELPGVLFGEWGLQELMLNFTQLRTL 306  
 QY 163 ---LRGTRRLRAGNT---RIAQRPEDLAGLAALQELDV----- 196  
 DB 307 AAAPRNLRLRYLGVTLSPRLSALPGARQGLQVLAHNSGLTALPDGLRGLKLR 366  
 QY 197 -----SNLS-----LQALPGLSGLFPRRLILAAARNPFCV 228  
 DB 367 QVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLPGDVFGALPRLTEVLIGHNSWRCD 426  
 QY 229 CPLSWGPGWVRESHTVLASPEE-TRCHFPKRNAGRLLELDVADFGCPATTTATVPTTR 287  
 DB 427 CGIGPPLGWLRC-HLVLVGSEEPRCAGRAHGLPLMLPGSDACPG-----PRGP 478  
 QY 288 PVREPTALSSSLAFTWLSPTAPTEAPSPSPAPPTVGP 327  
 DB 479 P--PRPAADSS-----BAPVHPALAPNSSE 503

RESULT 14  
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 neuronal leucine-rich repeat protein-3 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C/Accession: JC7763  
 R.Fukunishi, K.; Matsuka, Y.; Kitahara, C.; Kuchino, Y.; Tsuda, H.  
 Biochem. Biophys. Res. Commun. 287, 257-263, 2001  
 A/Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene  
 A/Reference number: JC7763; PMID:11549284  
 A/Contents: Fibrosarcoma cells  
 A/Accession: JC7763  
 A.Molecule type: mRNA  
 A.Residues: 1-707 <FUK>  
 A/Cross-references: UNIPROT:Q9ESY6; UNIPARC:UPI00004F0F2; GB:AF291437  
 C/Comment: This protein, a new member of the neuronal leucine-rich repeat protein family,  
 in protein-protein interaction and functions as a cell adhesion molecule or soluble ligar  
 C/Genetics:  
 A/Gene: nlr-3  
 C/Keywords: cell adhesion

Query Match 7.6%; Score 237; DB 2; Length 707;  
 Best Local Similarity 20.7%; Pred. No. 2e-06;  
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 DB 5 PLQIHVLGLATATVQAGDKKVCPCLOCTCELRPFTPRSIYMEASTVDCNDLGLNFP 64  
 QY 48 RQVPEPTVGLYFENGITWLDSSPAGLPGQLDLDSQNI----- 91  
 DB 65 ARUPADTQILLQTNRIARHST--DFPNVLGLDLSQNNSSVTNINVQKMSQLSVY 122  
 QY 92 -----RLPRLLLDLS-----HNSLLALEPIL----- 114

Db 123 LEENKITEPEKCLYGLSLNQLLYVNNHLLSAISPGAFVGLHLLRLHLNLSRLQWINSK 182  
QY 115 ---DTANVEALRL-----AGLQLODLGLFSRLNHLDL 147  
Db 183 WFEALFNLEILMLGDNPIRLKDMFQPLKLRSLVIAGINLVEPDDALVGLNLESIS 242  
QY 148 VSDNQLERVP-----PVIRLGR----- 165  
Db 243 FYDNRNKKVPOVALQKAVNLKFLDLNKNPINRIRRGDFSNMHLKELGINNMPPELVIDS 302  
QY 166 -----LTRLRAGNTRIAQLRPEDLAGLAALQELDVNSLSLOAL-PCDLSGLPRRLR 216  
Db 303 LAVDNLPLDLKRIEATNPNRLSYIHPNAPFLPKLESLMNSALSALYHGHTIESL-PNLK 361  
QY 217 LIAAARNPNCVCPPLSGFPGWFWRESHVTLASPEETRCHFPFKNAGRLLELDVADFCPA 276  
Db 362 EISIHNPICDCVIRIN--MKNTRIRFMEPSLFCVDPPEFGQGVNRQVHFRDM---- 415  
QY 277 TTTTATVPTTRPVVREPTALSSSL---APTWLSPATAPSPPTAPPTVGPVQPOPD 333  
Db 416 -----MEICLPLI-APESFPSILDVEADSVVSLHCRATAEPQ-----PEIYWIITPSGKR 463  
QY 334 CPSTCLNGGTCHL-GTRHHLACLCPGFTGLY---CESOMGQGTSPSPPTVTPRPPR-- 387  
Db 464 LLENTILREKFYVHSEGTLDIRGITPKEG--GLYTCIATNLVAGDLKSIMIKVGVFPQDN 521  
QY 388 --SLTLGIEPVSPSLRVLGRLQVLSQSSVQLRSRLTYRNLSGPDKELVTLRLPASLAEY 445  
Db 522 NGSNLKIRDIRANSVLVS---WKANSKILKSSVKWTAFTVKTEDSQAAQSARIPSDVKVY 578  
QY 446 TVTQLRPNATYVVCV 460  
Db 579 NLTHLPSTPEYKICI 593

RESULT 15  
T42626  
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)  
N:Alternate names: neurogenic extracellular slit protein  
C:Species: Mus musculus (house mouse)  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T42626  
R:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.  
Mech. Dev. 79, 57-72, 1998  
A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in  
A:Reference number: Z22177; MUID:9279238; PMID:10349621  
A:Accession: T42626  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1025 <HOL>  
A:Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI00000E8104; EMBL:AF074960; NID:G4151258;  
C:Genetics:  
A:Gene: Slit2  
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x

Query Match 7.4%; Score 231; DB 2; Length 1025;  
Best Local Similarity 24.0%; Pred. No. 6.9e-06;  
Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;

QY 24 CPSCGCSQPQTVECTARQGTTPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLIDL 83  
Db 223 CPSECTCLD-TXVRCNSKGLKVLPGIPKDVTELYLDGNQFTLV-PKELSNYKHLTLIDL 280  
QY 84 SQNOIASL-----RLPRLLLLDLSHNSLLALEPGILDITANVEALRAGLQLODGLF 137  
Db 281 SNNRISTLSNQXFSNMTQLTLILSYNRLRCIPRPTFD-----GLKSL----- 323  
QY 138 SRLNHLDLVDSDNQLSERVPPVIRGLRGLRFLRAGNTRIAQLRPEDLAGLAALQELDVS 197  
Db 324 -RLSLHGNDIS-----VVP----- 337  
QY 198 NLSLQALPGDLSGLFPRLRLAAARNPNCVPLSWFPGWFWRESHVTLASPEETRCHFP 257

Search completed: August 29, 2007, 08:49:23  
Job time : 69 secs

Db 338 -----EGAFNDLSA-----LSHLAIGANPLYCDCNMQWLSDWVKSEY----KEPGIARCAGPG 386  
QY 258 KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPATAPATEAPSP 317  
Db 387 EMADKLLLTTPSKKFTCQ-----GPMWITTIQAKCNPCLSN 421  
QY 318 PSTAPPTVGPVP-----QPQDCP-----PSTCLNGGTCHL--GTRHHLACL 356  
Db 422 PKNDGTCNNDPVDVFRCTCPYGFKGQDCDVPFHACISNPKHGCTCHLKEGENAGFWCT 481  
QY 357 CPSEGTGLYCE 367  
Db 482 CADGFEENCE 492

251	238.5	7.6	995	2	Q29KV3_DROPS	Q29kv3 drosophila	324	228	7.3	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
252	238	7.6	323	2	Q4RP13_9PETR	Q4rp13 ichtthyomyzo	325	228	7.3	322	2	Q32QP0_EPTST	Q32qp0 eptaretus
253	238	7.6	348	2	Q2YE73_EPTST	Q2ye73 eptaretus	326	228	7.3	838	2	Q4SPF9_TETNG	Q4spf9 tetraodon n
254	238	7.6	453	2	Q86XY1_HUMAN	Q86xy1 homo sapien	327	227.5	7.3	356	2	Q8BXQ3_MOUSE	Q8bxq3 m adult ret
255	238	7.6	544	2	Q8UV23_9PERC	Q8uv23 spherooides	328	227	7.2	311	1	LRC55_MOUSE	Q3uy51 mus muscul
256	237.5	7.6	323	2	Q2VE74_EPTST	Q2ve74 eptaretus	329	227	7.2	311	1	LRC55_RAT	Q4kl13 rattus norv
257	237.5	7.6	346	2	Q32R39_EPTBU	Q32r39 eptaretus	330	227	7.2	321	2	Q32R27_EPTBU	Q32r27 eptaretus
258	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9d3k0 m 6 days ne	331	227	7.2	344	2	Q2YE58_EPTST	Q2ye58 eptaretus
259	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4s4c0 tetraodon n	332	227	7.2	371	2	Q32R26_EPTBU	Q32r26 eptaretus
260	237	7.6	289	2	Q4KP06_LAMAP	Q4kp06 lampetra ap	333	227	7.2	783	2	Q90XG2_CHICK	Q90xg2 gallus gall
261	237	7.6	370	2	Q8N967_HUMAN	Q8n967 homo sapien	334	227	7.2	950	2	Q90Z44_CHICK	Q90z44 gallus gall
262	237	7.6	578	1	LRC15_FAT	Q8rm53 rattus norv	335	226.5	7.2	209	2	Q2VGN5_PETMA	Q2vgn5 petromyzo
263	237	7.6	707	1	LRRN3_RAT	Q9esy6 rattus norv	336	226.5	7.2	283	2	Q4G111_EPTST	Q4g111 eptaretus
264	237	7.6	1046	2	Q7PEZJ7_ANOGA	Q7pe27 xenopus lae	337	226.5	7.2	298	2	Q4KP16_9PETR	Q4kp16 ichtthyomyzo
265	236.5	7.5	461	2	Q4SA12_TETNG	Q4sa12 anopheles g	338	226.5	7.2	289	2	Q4KP19_EPTST	Q4kp19 ichtthyomyzo
266	236.5	7.5	715	2	Q4RY04_TETNG	Q4ry04 tetraodon n	339	226.5	7.2	323	2	Q32Q01_EPTST	Q32q01 eptaretus
267	236	7.5	306	2	Q2VDZ7_EPTST	Q2vdz7 eptaretus	340	226.5	7.2	557	1	LG11_HUMAN	Q95970 homo sapien
268	236	7.5	707	1	LRRN3_MOUSE	Q8cbc6 mus musculu	341	226.5	7.2	557	1	Q1EG12_PANTR	Q1eg12 pan troglod
269	236	7.5	718	2	Q6PEZ7_XENLA	Q6pe27 xenopus lae	342	226.5	7.2	719	1	LRFN5_HUMAN	Q96n16 homo sapien
270	235.5	7.5	283	2	Q2YE20_EPTST	Q2ye20 eptaretus	343	226	7.2	321	2	Q4KP16_9PETR	Q4kp16 ichtthyomyzo
271	235.5	7.5	296	2	Q4G1H6_EPTST	Q4g1h6 eptaretus	344	226	7.2	322	2	Q32QN1_EPTST	Q32qn1 eptaretus
272	235.5	7.5	307	2	Q2YE19_EPTST	Q2ye19 eptaretus	345	226	7.2	364	2	Q4SQ63_TETNG	Q4sq63 tetraodon n
273	235.5	7.5	307	2	Q2VE00_EPTST	Q2ve00 eptaretus	346	225.5	7.2	210	2	Q4SCF1_TETNG	Q4scf1 tetraodon n
274	235.5	7.5	579	1	LRC15_MOUSE	Q80x72 mus musculu	347	225.5	7.2	257	2	Q2VGS2_PETMA	Q2vgs2 petromyzo
275	235	7.5	574	2	Q4RRR5_TETNG	Q4rrr5 tetraodon n	348	225.5	7.2	298	2	Q6BAJ3_PETMA	Q6eaj3 petromyzo
276	234.5	7.5	346	2	Q32R33_EPTBU	Q32r33 eptaretus	349	225	7.2	733	2	Q2M032_DROPS	Q2m032 drosophila
277	234.5	7.5	488	2	Q4RK86_TETNG	Q4rk86 tetraodon n	350	224.5	7.2	323	2	Q32Q00_EPTST	Q32q00 eptaretus
278	234.5	7.5	703	2	Q16TC8_AEDAE	Q16tc8 aedes aegyp	351	224.5	7.2	347	2	Q32Q00_EPTST	Q32q00 eptaretus
279	234.5	7.5	958	2	Q29LE3_DROPS	Q29le3 drosophila	352	224	7.1	218	2	Q2VGM8_PETMA	Q2vgm8 petromyzo
280	233.5	7.4	298	2	Q6BAJ4_PETMA	Q6eaj4 petromyzo	353	224	7.1	322	2	Q32QR2_EPTST	Q32qr2 eptaretus
281	233.5	7.4	322	2	Q32QZ1_EPTBU	Q32qz1 eptaretus	354	224	7.1	1202	2	Q291L6_DROPS	Q291l6 drosophila
282	233.5	7.4	346	2	Q32QY9_EPTBU	Q32qy9 eptaretus	355	223.5	7.1	209	2	Q2VXG5_PETMA	Q2vxx5 petromyzo
283	233.5	7.4	545	2	Q5R534_PONPY	Q5r534 pongo pygma	356	223.5	7.1	283	2	Q4G1H8_EPTST	Q4g1h8 eptaretus
284	233.5	7.4	1587	2	Q17FD9_AEDAE	Q17fd9 aedes aegyp	357	223.5	7.1	323	2	Q2YE55_EPTST	Q2ye55 eptaretus
285	233	7.4	393	2	Q32R29_EPTBU	Q32r29 eptaretus	358	223.5	7.1	323	2	Q32Q00_EPTST	Q32q00 eptaretus
286	233	7.4	1316	2	Q9VQ25_DROME	Q9vq25 drosophila	359	223.5	7.1	647	2	Q64215_MOUSE	Q64215 mus musculu
287	232.5	7.4	323	2	Q2YE85_EPTST	Q2ye85 eptaretus	360	223	7.1	289	2	Q6E4C8_PETMA	Q6e4c8 petromyzo
288	232	7.4	487	2	Q4SA13_TETNG	Q4sa13 tetraodon n	361	223	7.1	345	2	Q2YE83_EPTBU	Q2ye83 eptaretus
289	232	7.4	766	2	Q2WF71_MOUSE	Q2wf71 mus musculu	362	223	7.1	349	2	Q4SH52_TETNG	Q4sh52 tetraodon n
290	231.5	7.4	283	2	Q4G1H4_EPTST	Q4g1h4 eptaretus	363	222.5	7.1	323	2	Q32QW5_EPTST	Q32qw5 eptaretus
291	231.5	7.4	323	2	Q2XE66_EPTST	Q2xe66 eptaretus	364	222.5	7.1	323	2	Q32QW5_EPTST	Q32qw5 eptaretus
292	231.5	7.4	323	2	Q32Q09_EPTST	Q32q09 eptaretus	365	222.5	7.1	323	2	Q32QV2_EPTST	Q32qv2 eptaretus
293	231.5	7.4	598	2	Q2PFR9_MACFA	Q2pf9 macaca fasc	366	222.5	7.1	413	2	Q64215_MOUSE	Q64215 mus musculu
294	231.5	7.4	840	1	SLIK6_MOUSE	Q8cl10 mus musculu	367	222.5	7.1	557	1	LG11_RAT	Q8k4y5 rattus norv
295	231	7.4	294	2	Q5VT95_HUMAN	Q5vt95 homo sapien	368	222.5	7.1	557	2	Q5R945_PONPY	Q5r945 pongo pygma
296	231	7.4	324	2	Q32QP7_EPTST	Q32qp7 eptaretus	369	222.5	7.1	557	2	Q5FWS7_RAT	Q5fws7 rattus norv
297	231	7.4	347	2	Q32R08_EPTBU	Q32r08 eptaretus	370	222.5	7.1	792	2	Q90Z43_CHICK	Q90z43 gallus gall
298	231	7.4	547	1	CPN2_MOUSE	Q9d3b9 mus musculu	371	222	7.1	269	2	Q6E4L0_PETMA	Q6e4l0 petromyzo
299	231	7.4	581	2	Q495Q6_HUMAN	Q495q6 homo sapien	372	222	7.1	348	2	Q95J18_MACFA	Q95j18 macaca fasc
300	231	7.4	619	2	Q7OBW2_ANOGA	Q7obw2 anopheles g	373	222	7.1	348	2	Q32QP2_EPTST	Q32qp2 eptaretus
301	231	7.4	766	2	Q4G0M4_MOUSE	Q4g0m4 mus musculu	374	222	7.1	348	2	Q32QN3_EPTST	Q32qn3 eptaretus
302	231	7.4	787	2	Q4SW26_TETNG	Q4sw26 tetraodon n	375	222	7.1	722	2	Q5PPU2_XENLA	Q5ppu2 xenopus lae
303	230.5	7.4	257	2	Q2VGP9_PETMA	Q2vgp9 petromyzo	376	221.5	7.1	249	2	Q2VXG2_PETMA	Q2vxg2 petromyzo
304	230.5	7.4	323	2	Q32Q03_EPTST	Q32q03 eptaretus	377	221.5	7.1	323	2	Q32QV6_EPTST	Q32qv6 eptaretus
305	230.5	7.4	687	2	Q4SCX3_TETNG	Q4scx3 tetraodon n	378	221.5	7.1	323	2	Q32QW6_EPTST	Q32qw6 eptaretus
306	230	7.3	332	2	Q8QFN7_ELAQU	Q8qfn7 elaphe quad	379	221.5	7.1	475	2	Q4T109_TETNG	Q4t109 tetraodon n
307	230	7.3	332	2	Q8QFN6_ELAQU	Q8qfn6 elaphe quad	380	221.5	7.1	557	1	LG11_MOUSE	Q9jia1 mus musculu
308	230	7.3	872	2	Q4SZ04_TETNG	Q4sz04 tetraodon n	381	221.5	7.1	719	1	LRFN5_MOUSE	Q8bxa0 mus musculu
309	230	7.3	1229	2	Q4T7S0_TETNG	Q4t7s0 tetraodon n	382	221.5	7.1	721	2	Q5DTH4_MOUSE	Q5dth4 mus musculu
310	229.5	7.3	233	2	Q2VGE3_PETMA	Q2vge3 petromyzo	383	221	7.0	286	2	Q2YE07_EPTST	Q2ye07 eptaretus
311	229.5	7.3	323	2	Q2VE65_EPTST	Q2ve65 eptaretus	384	221	7.0	322	2	Q32Q29_EPTST	Q32q29 eptaretus
312	229.5	7.3	323	2	Q2VE70_EPTST	Q2ve70 eptaretus	385	221	7.0	348	2	Q32Q07_EPTST	Q32q07 eptaretus
313	229.5	7.3	323	2	Q32QW0_EPTST	Q32qw0 eptaretus	386	221	7.0	348	2	Q32Q07_EPTST	Q32q07 eptaretus
314	229.5	7.3	370	2	Q32R18_EPTBU	Q32r18 eptaretus	387	221	7.0	1093	1	LRI1_HUMAN	Q96jai homo sapien
315	229.5	7.3	828	2	Q8C8T7_MOUSE	Q8c8t7 mus musculu	388	220.5	7.0	1528	2	Q2UZU6_AEDAE	Q2uzu6 aedes aegyp
316	229	7.3	240	2	Q2VGN7_PETMA	Q2vgn7 petromyzo	389	220.5	7.0	210	2	Q6E4M1_PETMA	Q6e4m1 petromyzo
317	229	7.3	324	2	Q32Q05_EPTST	Q32q05 eptaretus	390	220.5	7.0	306	2	Q4KP04_LAMAP	Q4kp04 lampetra ap
318	229	7.3	347	2	Q32R44_EPTBU	Q32r44 eptaretus	391	220.5	7.0	322	2	Q6E4K1_PETMA	Q6e4k1 petromyzo
319	229	7.3	348	2	Q32QW2_EPTST	Q32qw2 eptaretus	392	220.5	7.0	323	2	Q32QN5_EPTST	Q32qn5 eptaretus
320	229	7.3	581	1	LRC15_HUMAN	Q8etf66 homo sapien	393	220.5	7.0	342	2	Q4RW94_TETNG	Q4rw94 tetraodon n
321	228.5	7.3	294	2	Q6B4L6_PETMA	Q6b4l6 petromyzo	394	220.5	7.0	515	1	LRTM2_MOUSE	Q8bga3 mus musculu
322	228.5	7.3	341	1	LRC55_HUMAN	Q6zba7 homo sapien	395	220.5	7.0	515	2	Q8C8L1_MOUSE	Q8c8l1 mus musculu
323	228.5	7.3	342	2	Q4RRU5_TETNG	Q4rru5 tetraodon n	396	220.5	7.0	733	2	Q24250_DROME	Q24250 drosophila

397	220.5	7.0	841	1	SLIK6_HUMAN	Q9h5v7	homo sapien	470	213.5	6.8	1204	2	Q17K70_AEDAE	O17k70	aedes aegyp
398	220	7.0	345	2	Q32R13_EPTBU	Q32r13	eptaretus	471	213	6.8	218	2	Q2VCT0_PETWA	Q2vct0	petromyzon
399	220	7.0	347	2	Q32R23_EPTBU	Q32r23	eptaretus	472	213	6.8	322	2	Q32OX1_EPTST	Q32ox1	eptaretus
400	220	7.0	582	1	LRTM3_MOUSE	Q8bz81	mus musculus	473	213	6.8	327	2	Q32QZ5_EPTBU	Q32qz5	eptaretus
401	220	7.0	582	2	Q8BZA0_MOUSE	Q8bza0	mus musculus	474	213	6.8	343	2	Q32R04_EPTBU	Q32r04	eptaretus
402	220	7.0	603	2	Q4S2J27_TETNG	Q4s2j27	tetraodon n	475	213	6.8	716	1	LRRN1_MOUSE	Q61809	mus musculus
403	219.5	7.0	323	2	Q32Q33_EPTST	Q32q33	eptaretus	476	213	6.8	811	2	Q17JT2_AEDAE	O17jt2	aedes aegyp
404	219.5	7.0	323	2	Q32Q74_EPTST	Q32q74	eptaretus	477	212.5	6.8	323	2	Q32Q53_EPTST	Q32q53	eptaretus
405	219.5	7.0	323	2	Q32QW4_EPTST	Q32qw4	eptaretus	478	212.5	6.8	604	2	Q4SHE8_TETNG	Q4she8	tetraodon n
406	219.5	7.0	323	2	Q32QV3_EPTST	Q32qv3	eptaretus	479	212	6.8	216	2	Q2VGH4_PETWA	Q2vgh4	petromyzon
407	219.5	7.0	583	2	Q4SNQ0_TETNG	Q4snq0	tetraodon n	480	212	6.8	218	2	Q2VGI6_PETWA	Q2vgi6	petromyzon
408	219	7.0	218	2	Q2VH13_PETWA	Q2vhl3	petromyzon	481	212	6.8	276	2	Q4GIJ9_EPTST	Q4gij9	eptaretus
409	219	7.0	264	2	Q2VH48_PETWA	Q2vh48	petromyzon	482	212	6.8	324	2	Q32QW9_EPTST	Q32qw9	eptaretus
410	219	7.0	324	2	Q2VH60_EPTST	Q2vhe60	petromyzon	483	212	6.8	445	1	R4RL1_RAT	Q80wd0	rattus norv
411	219	7.0	334	2	Q6P7C4_RAT	Q6p7c4	rattus norv	484	212	6.8	918	2	Q7Q3F0_ANOGA	Q7q3f0	anopheles g
412	218.5	7.0	322	2	Q2VGH7_PETWA	Q2vgh7	petromyzon	485	211.5	6.7	192	2	Q6E419_PETWA	Q6e419	petromyzon
413	218.5	7.0	323	2	Q2VE76_EPTST	Q2ve76	eptaretus	486	211.5	6.7	270	2	Q6E417_PETWA	Q6e417	petromyzon
414	218.5	7.0	359	2	Q6GTU0_HUMAN	Q6gtu0	homo sapien	487	211.5	6.7	322	2	Q32R35_EPTBU	Q32r35	eptaretus
415	218.5	7.0	618	1	LRC21_MOUSE	Q8k099	mus musculus	488	211.5	6.7	323	2	Q2YE72_EPTST	Q2ye72	eptaretus
416	218	7.0	216	2	Q2VGH7_PETWA	Q2vgh7	petromyzon	489	211.5	6.7	323	2	Q32QW9_EPTST	Q32qw9	eptaretus
417	218	7.0	264	2	Q2VGT2_PETWA	Q2vgt2	petromyzon	490	211.5	6.7	323	2	Q32Q57_EPTST	Q32q57	eptaretus
418	218	7.0	323	2	Q32R09_EPTBU	Q32r09	eptaretus	491	211.5	6.7	518	2	Q5R712_PONPY	Q5r712	pongo pygma
419	218	7.0	347	2	Q32R14_EPTBU	Q32r14	eptaretus	492	211.5	6.7	876	2	Q16L90_AEDAE	O16l90	aedes aegyp
420	217.5	6.9	288	2	Q8BR15_MOUSE	Q8br15	mus musculus	493	211	6.7	197	2	Q6E412_PETWA	Q6e412	petromyzon
421	217.5	6.9	615	2	Q4SLU7_TETNG	Q4slu7	tetraodon n	494	211	6.7	218	2	Q2VGR7_PETWA	Q2vgr7	petromyzon
422	217.5	6.9	695	2	Q4TLY8_TETNG	Q4tly8	tetraodon n	495	211	6.7	581	1	LRTM3_HUMAN	Q86vh5	homo sapien
423	217.5	6.9	1335	2	Q610C7_CAEBR	Q610c7	caenorhabdi	496	211	6.7	581	1	LRTM3_HUMAN	Q9b9p6	macaca fasc
424	217	6.9	322	2	Q2YB64_EPTST	Q2yeb4	eptaretus	497	211	6.7	581	2	Q2NKK7_HUMAN	Q2nkk7	homo sapien
425	217	6.9	348	2	Q32Q4_EPTST	Q32q4	eptaretus	498	210.5	6.7	209	2	Q2VGR9_PETWA	Q2vgr9	petromyzon
426	217	6.9	637	2	Q6DCV7_XENIA	Q6dcv7	xenopus lae	499	210.5	6.7	257	2	Q4GIM3_EPTBU	Q4gim3	eptaretus
427	216.5	6.9	209	2	Q2VGT8_PETWA	Q2vgt8	petromyzon	500	210.5	6.7	321	2	Q6E4L5_PETWA	Q6e4l5	petromyzon
428	216	6.9	263	2	Q6E4C7_PETWA	Q6e4c7	petromyzon	501	210.5	6.7	322	2	Q32R37_EPTBU	Q32r37	eptaretus
429	216	6.9	282	2	Q4G1I6_EPTST	Q4g1i6	eptaretus	502	210.5	6.7	322	2	Q32R10_EPTBU	Q32r10	eptaretus
430	216	6.9	324	2	Q32QW1_EPTST	Q32qw1	eptaretus	503	210.5	6.7	4303	1	PKD1_HUMAN	P8161	homo sapien
431	216	6.9	324	2	Q32Q54_EPTST	Q32q54	eptaretus	504	210	6.7	264	2	Q2VGI2_PETWA	Q2vgi2	petromyzon
432	216	6.9	514	2	Q4VXB1_MOUSE	Q4vxb1	mus musculus	505	210	6.7	324	2	Q2YE50_EPTST	Q2ye50	eptaretus
433	215.5	6.9	322	2	Q32R32_EPTBU	Q32r32	eptaretus	506	210	6.7	324	2	Q32Q04_EPTST	Q32q04	eptaretus
434	215.5	6.9	323	2	Q32Q76_EPTST	Q32q76	eptaretus	507	210	6.7	324	2	Q32Q70_EPTST	Q32q70	eptaretus
435	215.5	6.9	323	2	Q2YB61_EPTST	Q2yeb1	eptaretus	508	210	6.7	324	2	Q32Q52_EPTST	Q32q52	eptaretus
436	215.5	6.9	329	2	Q56NG5_CIOIN	Q56ng5	ciona intes	509	210	6.7	358	1	CHAD_RAT	O70210	rattus norv
437	215.5	6.9	331	1	PLIB_AGBL	Q93233	agkistrodon	510	210	6.7	1028	2	Q865R7_PIG	Q865r7	sus scrofa
438	215.5	6.9	612	2	Q4SYK9_TETNG	Q4syk9	tetraodon n	511	209.5	6.7	214	2	Q6E4H0_PETWA	Q6e4h0	petromyzon
439	215.5	6.9	737	2	Q9VU51_DROME	Q9vu51	drosophila	512	209.5	6.7	322	2	Q32R06_EPTBU	Q32r06	eptaretus
440	215	6.9	322	2	Q32QX8_EPTST	Q32qx8	eptaretus	513	209.5	6.7	322	2	Q32R12_EPTBU	Q32r12	eptaretus
441	215	6.9	323	2	Q2YB53_EPTST	Q2yeb3	eptaretus	514	209.5	6.7	323	2	Q32Q08_EPTST	Q32q08	eptaretus
442	215	6.9	323	2	Q32QY8_EPTBU	Q32qy8	eptaretus	515	209.5	6.7	323	2	Q32Q51_EPTST	Q32q51	eptaretus
443	215	6.9	323	2	Q32R00_EPTBU	Q32r00	eptaretus	516	209.5	6.7	323	2	Q32Q06_EPTST	Q32q06	eptaretus
444	215	6.9	323	2	Q32Q00_EPTST	Q32q00	eptaretus	517	209.5	6.7	382	2	Q1EGK9_PANTR	Q1egk9	pan troglod
445	215	6.9	324	2	Q32Q04_EPTST	Q32q04	eptaretus	518	209.5	6.7	533	2	Q5E9T6_BOVIN	Q5e9t6	bos taurus
446	214.5	6.8	743	2	Q6PIM7_HUMAN	Q6pim7	homo sapien	519	209	6.7	211	2	Q6E413_PETWA	Q6e413	petromyzon
447	214.5	6.8	215	2	Q2VH33_PETWA	Q2vhl3	petromyzon	520	209	6.7	216	2	Q2VGO6_PETWA	Q2vgo6	petromyzon
448	214.5	6.8	323	2	Q32Q84_EPTST	Q32q84	eptaretus	521	209	6.7	257	2	Q6E4J6_PETWA	Q6e4j6	petromyzon
449	214.5	6.8	323	2	Q32Q86_EPTST	Q32q86	eptaretus	522	209	6.7	322	2	Q32QW8_EPTST	Q32qw8	eptaretus
450	214.5	6.8	323	2	Q32QP5_EPTST	Q32qp5	eptaretus	523	209	6.7	323	2	Q32R01_EPTBU	Q32r01	eptaretus
451	214.5	6.8	329	2	Q56NG6_CIOIN	Q56ng6	ciona intes	524	209	6.7	358	1	CHAD_MOUSE	Q55226	mus musculus
452	214.5	6.8	347	2	Q32QP1_EPTST	Q32qp1	eptaretus	525	209	6.7	358	2	Q5SVU4_MOUSE	Q5svu4	mus musculus
453	214.5	6.8	441	1	R4RL1_HUMAN	Q86un2	homo sapien	526	209	6.7	391	2	Q4SBB7_TETNG	Q4sbb7	tetraodon n
454	214.5	6.8	716	1	LRRN1_MOUSE	Q8uxx5	homo sapien	527	209	6.7	1091	1	LRI61_MOUSE	P70193	mus musculus
455	214.5	6.8	731	2	Q4T149_TETNG	Q4t149	tetraodon n	528	209	6.7	1262	1	Q29L45_DROPS	Q29l45	drosophila
456	214.5	6.8	1535	2	Q32391_DROME	Q32391	drosophila	529	208.5	6.7	350	2	Q5RH06_BRARE	Q5rh06	brachydanio
457	214	6.8	295	2	Q6E4C9_PETWA	Q6e4c9	petromyzon	530	208.5	6.7	382	1	PRELP_HUMAN	P51888	homo sapien
458	214	6.8	323	2	Q32R42_EPTBU	Q32r42	eptaretus	531	208.5	6.7	382	2	Q6FHG6_HUMAN	Q6fhg6	homo sapien
459	214	6.8	324	2	Q2YB68_EPTST	Q2yeb8	eptaretus	532	208.5	6.7	382	2	Q6FG38_HUMAN	Q6fg38	homo sapien
460	214	6.8	516	1	LRTM2_HUMAN	Q43300	homo sapien	533	208.5	6.7	445	1	R4RL1_MOUSE	Q8k085	mus musculus
461	214	6.8	716	1	LRRN1_RAT	Q32q07	rattus norv	534	208.5	6.7	479	2	Q6X3Y5_BRARE	Q6x3y5	brachydanio
462	214	6.8	717	2	Q4SR34_TETNG	Q4sr34	tetraodon n	535	208.5	6.7	518	1	LRTM4_HUMAN	Q86vh4	homo sapien
463	214	6.8	2828	2	Q9NR99_HUMAN	Q9nr99	homo sapien	536	208.5	6.7	518	2	Q4FZ98_HUMAN	Q4fz98	homo sapien
464	213.5	6.8	238	2	Q6E4J5_PETWA	Q6e4j5	petromyzon	537	208.5	6.7	519	2	Q4KXK1_HUMAN	Q4kxk1	homo sapien
465	213.5	6.8	259	2	Q2YB23_EPTST	Q2yeb23	eptaretus	538	208.5	6.7	537	1	LGI14_HUMAN	Q8n135	homo sapien
466	213.5	6.8	273	2	Q4G1I2_EPTBU	Q4g1i2	eptaretus	539	208.5	6.7	590	2	Q6UXJ7_HUMAN	Q6uxj7	homo sapien
467	213.5	6.8	323	2	Q32QW9_EPTST	Q32qw9	eptaretus	540	208	6.6	218	2	Q2VGF5_PETWA	Q2vgf5	petromyzon
468	213.5	6.8	359	1	CHAD_HUMAN	O15335	homo sapien	541	208	6.6	322	2	Q2YB51_EPTST	Q2yeb51	eptaretus
469	213.5	6.8	361	1	CHAD_BOVIN	Q27972	bos taurus	542	208	6.6	649	2	Q9VK22_DROME	Q9vk22	drosophila

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: August 29, 2007, 08:48:45 ; Search time 343 Seconds  
(without alignments)  
1869.185 Million cell updates/sec  
Title: US-09-943-780-69  
Perfect score: 3135  
Sequence: 1 MCSRVPLLLPLLLLALGPG.....PLMGPPGGLQSLHAKPYI 598  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 3281787 seqs, 1072124677 residues  
Total number of hits satisfying chosen parameters: 3281787  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries  
Database : UniProt\_8.4.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3078.5	98.2	673	1 VASN_HUMAN	Q6mk4 homo sapien
2	2490	79.4	673	1 VASN_MOUSE	Q6czt5 mus musculus
3	1213.5	38.7	561	1 VASN_XENTR	Q6df55 xenopus tro
4	972.5	31.0	688	2 Q3WKM9_BRARE	Q3mkx9 brachydanio
5	927.5	29.6	643	2 Q5Q3G2_BRARE	Q503g2 tetraodon n
6	914.5	29.2	962	2 Q4SQ68_TETNG	Q4sq68 tetraodon n
7	368.5	11.8	513	1 LRC24_HUMAN	Q501g9 homo sapien
8	359.5	11.5	635	1 LRFN4_HUMAN	Q6pi99 homo sapien
9	351	11.2	636	1 LRFN4_MOUSE	Q80x88 mus musculus
10	348	11.1	636	2 Q460G5_MOUSE	Q460g5 mus musculus
11	341	10.9	634	2 Q3UVS6_MOUSE	Q3uv56 mus musculus
12	341	10.9	660	2 Q8BLU0_MOUSE	Q8blu0 m adult mal
13	339	10.8	521	1 LRC24_MOUSE	Q8bba1 mus musculus
14	338	10.8	655	2 Q4SGV9_TETNG	Q4sgv9 tetraodon n
15	332	10.6	637	2 Q6A073_MOUSE	Q6a073 mus musculus
16	331.5	10.6	622	2 Q59GV4_HUMAN	Q59gv4 homo sapien
17	330	10.5	653	1 LRRG4_HUMAN	Q9hbw1 homo sapien
18	329.5	10.5	648	2 Q6DDY0_XENLA	Q6ddy0 xenopus lae
19	325.5	10.4	570	2 Q70AK2_XENLA	Q70ak2 xenopus lae
20	324	10.3	626	1 LRFN3_MOUSE	Q8bly3 mus musculus
21	324	10.3	626	2 Q505E2_MOUSE	Q505e2 mus musculus
22	323	10.3	732	2 Q4RPB8_TETNG	Q4rpb8 tetraodon n
23	322.5	10.3	682	2 Q6DJD2_XENLA	Q6ddj2 xenopus lae
24	322.5	10.3	811	2 Q7LOX0_HUMAN	Q7l0x0 homo sapien
25	322.5	10.3	887	2 Q75139_HUMAN	Q75139 homo sapien
26	322	10.3	605	1 ALS_PAPHA	Q02833 papio hamad
27	321.5	10.3	709	1 LRC4B_MOUSE	P0c192 mus musculus
28	321	10.2	628	1 LRFN3_HUMAN	Q9bnt0 homo sapien
29	321	10.2	762	2 Q5JY13_HUMAN	Q5jy13 homo sapien
30	320.5	10.2	597	2 Q310Y3_BOVIN	Q310y3 bos taurus
31	320	10.2	660	1 FLRT2_HUMAN	Q43155 homo sapien

Q6rkx8 m fibronect	674	2	Q6RXD8_MOUSE
Q58cs0 bos taurus	602	2	Q58CS0_BOVIN
Q45r42 rattus norv	652	2	Q45R42_RAT
Q99ph1 mus musculu	652	1	LRRCA_MOUSE
Q6nu16 homo sapien	778	36	317 10.1
Q1rm54 bos taurus	713	1	LRC4B_HUMAN
Q70ak3 xenopus lae	628	2	Q1RMS4_BOVIN
Q4sbt7 tetraodon n	648	2	Q70AK3_XENLA
Q7m620 mus musculu	935	2	Q4SBT7_TETNG
Q80wdl rattus norv	420	1	R4RL2_MOUSE
Q80zui homo sapien	420	1	R4RL2_RAT
Q8nc95 homo sapien	646	1	FLRT1_HUMAN
Q8nc95 homo sapien	627	2	O8NC95_HUMAN
Q9nz40 homo sapien	649	1	FLRT3_HUMAN
Q4tbm8 tetraodon n	649	2	Q54229_HUMAN
Q8wva2 homo sapien	626	2	Q4TBM8_TETNG
Q68f21 xenopus lae	674	2	O8WVA2_HUMAN
Q5r6t0 pongo pygma	637	2	Q68F21_XENLA
Q6php6 mus musculu	649	2	Q5R6T0_PONPY
Q6us92 mus musculu	730	2	Q6PHP6_MOUSE
Q46un3 homo sapien	692	2	Q6US92_MOUSE
Q86un3 homo sapien	420	1	Q4GOS0_HUMAN
Q17rl9 homo sapien	420	2	R4RL2_HUMAN
Q4shd7 tetraodon n	618	2	Q17RL5_HUMAN
P35858 homo sapien	605	1	Q4SHD7_TETNG
Q28256 canis famil	605	1	ALS_HUMAN
Q8bgl1 m 12 days e	649	2	Q8TAY0_HUMAN
Q8zpd1 mus musculu	663	2	Q28256_CANFA
Q8c031 mus musculu	640	1	O8BGT1_MOUSE
Q50517 brachydanio	640	2	Q6ZPQ1_MOUSE
Q499c1 brachydanio	647	2	NGLI_MOUSE
Q9dbv4 m adult mal	809	2	Q505E5_MOUSE
Q9ncj2 homo sapien	640	1	Q50317_BRARE
Q49622 rattus norv	811	2	Q9DBY4_MOUSE
Q80tv0 mus musculu	837	2	NGLI_HUMAN
Q7t2w3 brachydanio	372	2	Q49622_RAT
Q4sy17 tetraodon n	581	2	Q80TV0_MOUSE
Q4jwi0 homo sapien	640	2	Q7T2W3_BRARE
Q4s4w6 tetraodon n	428	2	Q4SY17_TETNG
Q4rq15 tetraodon n	713	1	Q4JIW0_HUMAN
Q75325 homo sapien	650	2	Q4S4W6_TETNG
Q4jiv9 homo sapien	640	2	LRRN5_HUMAN
Q6wzdl brachydanio	457	2	Q4RQ15_TETNG
Q5c0v4 homo sapien	782	2	Q4JIV9_HUMAN
Q70211 rattus norv	603	2	Q6WZD1_BRARE
Q9de37 brachydanio	1515	2	Q5T0V4_HUMAN
Q9p263 homo sapien	745	2	Q70211_RAT
Q92359 homo sapien	785	2	Q9DE37_BRARE
P35859 rattus norv	626	1	Q6UXK2_HUMAN
Q90245 gallus gall	603	1	Q9P263_HUMAN
Q4sr95 tetraodon n	738	2	GP1BA_HUMAN
Q2ydz4 eptatretus	633	2	ALS_RAT
Q57029 mus musculu	331	2	Q90245_CHICK
Q3kq39 mus musculu	619	2	Q4SR95_TETNG
Q791q5 mus musculu	603	1	Q2YDZ4_EPTST
Q9jil0 mus musculu	603	2	Q570Z9_MOUSE
Q6e4k4 petromyzon	687	2	Q3KQF3_MOUSE
Q88279 rattus norv	321	1	ALS_MOUSE
Q491k9 eptatretus	1531	1	Q9JIL0_MOUSE
Q3y6s4 brachydanio	330	2	Q6E4K4_PETMA
Q32qn8 eptatretus	1532	2	SLIT1_RAT
Q4rti6 tetraodon n	347	2	Q4G1K9_EPTBU
Q80tr4 mus musculu	1071	1	Q3Y6S4_BRARE
Q6wri0 homo sapien	1531	1	Q32QN8_EPTST
Q6yul1 eptatretus	2623	2	Q4RTI6_TETNG
Q6uy18 homo sapien	358	2	SLIT1_MOUSE
P24014 drosophila	593	2	Q6WRI0_HUMAN
Q5rkr3 mus musculu	1504	1	Q2YEO1_EPTST
	745	2	Q6UY18_HUMAN
	8.7	2	SLIT_DROME
	273	2	Q5RKR3_MOUSE
	273	2	



105	273	8.7	785	2	Q62PQ3_MOUSE	Q6zpq3 mus musculus	178	251	8.0	1021	2	Q9V430_DROME	Q9v430 drosophila
106	272.5	8.7	1524	2	Q3S2J2_BRARE	Q3s8j2 brachydanio	179	250	8.0	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
107	272	8.7	372	2	Q32QO2_EPTST	Q32qg2 eptaretus	180	249.5	8.0	347	2	Q32QO1_EPTST	Q32qo1 eptaretus
108	271.5	8.7	342	2	Q91X1L1_MOUSE	Q91xl1 mus musculus	181	249.5	8.0	789	1	LRFN2_HUMAN	Q9ulh4 homo sapien
109	271.5	8.7	347	2	Q32QO6_EPTST	Q32qg6 eptaretus	182	249.5	8.0	789	1	LRFN2_HUMAN	Q9be71 macaca fasc
110	271.5	8.7	1312	2	Q61PFO_CABER	Q61pf0 caenorhabdi	183	249.5	8.0	2597	2	Q6WRH5_RAT	Q6wrh9 rattus norv
111	271	8.6	372	2	Q32QO5_EPTST	Q32qg5 eptaretus	184	248.5	7.9	420	1	TPBG_MACFA	Q4r8y9 macaca fasc
112	271	8.6	473	1	RTN4R_HUMAN	Q9bzr6 homo sapien	185	248	7.9	284	2	Q2YE15_EPTST	Q2ye15 eptaretus
113	271	8.6	473	1	RTN4R_MACFA	Q9bzr6 homo sapien	186	248	7.9	481	1	NYX_HUMAN	Q9guu5 homo sapien
114	270.5	8.6	541	2	Q6PK41_HUMAN	Q6pk41 macaca fasc	187	248	7.9	481	1	Q2MIS4_HUMAN	Q9guu5 homo sapien
115	270	8.6	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio	188	247.5	7.9	305	2	Q4G1L3_EPTBU	Q4g1l3 eptaretus
116	270	8.6	1461	2	Q5VW18_HUMAN	Q5vw18 homo sapien	189	247.5	7.9	323	2	Q32QO7_EPTST	Q32qt7 eptaretus
117	270	8.6	1534	1	SLV1L1_HUMAN	Q5v033 homo sapien	190	247.5	7.9	323	2	Q32QO2_EPTST	Q32qt2 eptaretus
118	270	8.6	1534	2	Q5VW17_HUMAN	Q5v033 homo sapien	191	247.5	7.9	739	2	Q32QO2_EPTST	Q32qt2 eptaretus
119	268.5	8.6	409	2	Q5TQV2_HUMAN	Q5tv02 mus musculus	192	247.5	7.9	1521	1	SLIT2_MOUSE	Q2pnw3 xenopus lae
120	268	8.5	417	2	Q6E4J7_PETWA	Q6e4j7 petromyzon	193	247.5	7.9	1529	1	SLIT2_HUMAN	Q9rlb9 mus musculus
121	267.5	8.5	1512	2	Q9DE36_BRARE	Q9de36 brachydanio	194	247.5	7.9	1529	1	Q17RU3_HUMAN	Q94813 homo sapien
122	266.5	8.5	1529	2	Q7ZX12_XENLA	Q7zx12 xenopus lae	195	247.5	7.9	1530	2	Q90WZ3_XENLA	Q17ru3 homo sapien
123	266	8.5	460	2	Q6IP16_HUMAN	Q6ip16 homo sapien	196	247	7.9	794	2	Q4SK16_TETNG	Q90wz3 xenopus lae
124	266	8.5	734	2	Q3S930_MOUSE	Q3s930 mus musculus	197	247	7.9	1473	2	Q28WZ1_DROPS	Q4sk16 tetraodon n
125	265.5	8.5	1044	2	Q5ISR9_MACFA	Q5isr9 macaca fasc	198	246.5	7.9	283	2	Q2YE14_EPTST	Q28wz1 drosophila
126	265	8.5	298	2	Q4G1L7_EPTBU	Q4g1l7 eptaretus	199	246.5	7.9	323	2	Q2YE02_EPTST	Q2ye14 eptaretus
127	265	8.5	734	2	Q5SX47_MOUSE	Q5sx47 mus musculus	200	246.5	7.9	371	2	Q32QO6_EPTST	Q2ye02 eptaretus
128	264.5	8.4	420	1	TPBG_HUMAN	Q13641 mus musculus	201	246	7.8	284	2	Q2VGV6_PETWA	Q32qp6 eptaretus
129	264	8.4	334	2	Q2I0M4_HUMAN	Q2i0m4 homo sapien	202	246	7.8	306	2	Q2YE10_EPTST	Q2vqv6 petromyzon
130	264	8.4	334	2	Q5VSG2_HUMAN	Q5vsg2 homo sapien	203	246	7.8	308	2	Q4G1I3_EPTST	Q2ye10 eptaretus
131	264	8.4	352	2	Q4G1L1_EPTBU	Q4g1l1 eptaretus	204	246	7.8	346	2	Q2KIF2_BOVIN	Q4g1i3 eptaretus
132	263	8.4	308	2	Q2YDZ5_EPTST	Q2ydz5 eptaretus	205	245.5	7.8	331	2	Q3UUV1_MOUSE	Q2kif2 bos taurus
133	263	8.4	322	2	Q5I0E1_RAT	Q5i0e1 rattus norv	206	245.5	7.8	331	2	Q91W20_MOUSE	Q3uuv1 m 6 days ne
134	263	8.4	1253	2	Q4T0S1_TETNG	Q4t0s1 tetraodon n	207	245.5	7.8	346	2	Q32Q16_EPTBU	Q91w20 m cda sequ
135	262.5	8.4	1393	2	Q16WM1_AEDAE	Q16wm1 aedes aegypt	208	245.5	7.8	544	2	Q61X58_CABER	Q32q16 eptaretus
136	262	8.4	346	2	Q4G1L9_EPTBU	Q4g1l9 eptaretus	209	245.5	7.8	788	2	Q460M5_RAT	Q61x58 caenorhabdi
137	261.5	8.3	347	1	A2GL_HUMAN	P02750 homo sapien	210	245	7.8	306	2	Q4G1K6_EPTST	Q460m5 rattus norv
138	261	8.3	318	2	Q2YE28_EPTBU	Q2ye28 eptaretus	211	245	7.8	321	2	Q6E4T9_PETWA	Q4g1k6 eptaretus
139	261	8.3	341	2	Q2YE06_EPTST	Q2ye06 eptaretus	212	245	7.8	708	1	LRRN3_FONPY	Q6e4t9 petromyzon
140	261	8.3	1523	1	SLIT3_RAT	Q88280 rattus norv	213	244.5	7.8	411	2	Q4S6L6_TETNG	Q5r482 pongo pygma
141	260	8.3	306	2	Q2YE21_EPTST	Q2ye21 eptaretus	214	244.5	7.8	718	2	Q73675_XENLA	Q4s6l6 tetraodon n
142	259	8.3	370	2	Q2YE78_EPTST	Q2ye78 eptaretus	215	244.5	7.8	766	1	SLIT2_RAT	Q73675 xenopus lae
143	258	8.2	321	2	Q6E4D1_PETWA	Q6e4d1 petromyzon	216	244.5	7.8	788	1	LRFN2_MOUSE	Q9wvc1 rattus norv
144	258	8.2	370	2	Q2YE77_EPTST	Q2ye77 eptaretus	217	244.5	7.8	1593	2	Q5DTL5_MOUSE	Q80tg9 mus musculus
145	258	8.2	1523	1	SLIT3_HUMAN	Q75094 homo sapien	218	244	7.8	346	2	Q32QV4_EPTST	Q5dtl5 mus musculus
146	257.5	8.2	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n	219	244	7.8	458	2	Q6WZD3_BRARE	Q32qv4 eptaretus
147	257.5	8.2	347	2	Q32QX0_EPTST	Q32qx0 eptaretus	220	244	7.8	567	1	GPV_RAT	Q6wzd3 brachydanio
148	257.5	8.2	501	2	Q4SZC5_TETNG	Q4szc5 tetraodon n	221	244	7.8	708	1	LRRN3_HUMAN	Q08770 rattus norv
149	257	8.2	306	2	Q2YDZ6_EPTST	Q2ydz6 eptaretus	222	243.5	7.8	347	2	Q32QO8_EPTST	Q32qo8 eptaretus
150	257	8.2	473	1	RTN4R_RAT	Q99m75 rattus norv	223	243.5	7.8	476	1	NYX_MOUSE	Q83503 mus musculus
151	257	8.2	739	2	Q8BKW5_MOUSE	Q8bkms mus musculus	224	243	7.8	242	2	Q2VVGX4_PETWA	Q2vvgx4 petromyzon
152	256.5	8.2	342	2	Q4SGG5_TETNG	Q4sgg5 tetraodon n	225	243	7.8	290	2	Q2VVGX3_PETWA	Q2vvgx3 petromyzon
153	255.5	8.1	1095	2	Q90XG4_CHICK	Q90xg4 gallus gall	226	243	7.8	321	2	Q6E4L4_PETWA	Q6e4l4 petromyzon
154	254.5	8.1	1196	2	Q3V1M1_MOUSE	Q3v1m1 mus musculus	227	243	7.8	323	2	Q32QV0_EPTST	Q32qv0 eptaretus
155	254	8.1	528	2	Q8N644_HUMAN	Q8n644 homo sapien	228	242.5	7.7	355	2	Q2YB75_EPTST	Q2yb75 eptaretus
156	254	8.1	1523	1	SLIT3_MOUSE	Q9wv44 mus musculus	229	242.5	7.7	371	2	Q32QW7_EPTST	Q32qw7 eptaretus
157	254	8.1	1523	2	Q3UHN1_MOUSE	Q3uhn1 mus musculus	230	242.5	7.7	388	2	Q6ZM54_BRARE	Q6zm54 brachydanio
158	254	8.1	1523	2	Q5SS56_MOUSE	Q5ss56 mus musculus	231	242.5	7.7	545	1	CPN2_HUMAN	Q22792 homo sapien
159	253.5	8.1	347	2	Q68CK4_HUMAN	Q68ck4 homo sapien	232	242.5	7.7	718	2	Q6PCK4_XENLA	Q6pck4 xenopus lae
160	253.5	8.1	429	2	Q3UPM4_MOUSE	Q3upm4 mus musculus	233	242	7.7	220	2	Q2VGH4_PETWA	Q2vgh4 petromyzon
161	253.5	8.1	589	2	Q6GQU6_MOUSE	Q6gqu6 mus musculus	234	242	7.7	266	2	Q2VGF4_PETWA	Q2vgh4 petromyzon
162	253.5	8.1	1410	2	Q20204_CAEEL	Q20204 caenorhabdi	235	242	7.7	380	2	Q5TQV3_HUMAN	Q5tv03 homo sapien
163	253	8.1	368	2	Q32QF3_EPTST	Q32qf3 eptaretus	236	242	7.7	652	2	Q7PVZ3_ANOGA	Q7pvz3 anopheles g
164	253	8.1	426	1	TPBG_MOUSE	Q3u010 mus musculus	237	241.5	7.7	272	2	Q4KPI2_LAMAP	Q4kpi2 lampetra ap
165	253	8.1	426	2	Q3UP12_MOUSE	Q3up12 mus musculus	238	241.5	7.7	311	2	Q6E4L3_PETWA	Q6e4l3 petromyzon
166	253	8.1	567	1	GPV_MOUSE	Q08742 mus musculus	239	241	7.7	330	2	Q2YD29_EPTST	Q2yds9 eptaretus
167	252.5	8.1	323	2	Q2YE08_EPTST	Q2ye08 eptaretus	240	240.5	7.7	299	2	Q2YD23_EPTST	Q2yds3 eptaretus
168	252	8.0	311	2	Q6E4L1_PETWA	Q6e4l1 petromyzon	241	240.5	7.7	323	2	Q32QV1_EPTST	Q32qv1 eptaretus
169	252	8.0	426	1	TPBG_RAT	Q5pqv5 rattus norv	242	240.5	7.7	323	2	Q2YB62_EPTST	Q2yb62 eptaretus
170	252	8.0	567	2	Q3TA66_MOUSE	Q3ta66 mus musculus	243	240.5	7.7	323	2	Q32QX5_EPTST	Q32qx5 eptaretus
171	252	8.0	567	2	Q9QZU3_MOUSE	Q9qzu3 mus musculus	244	240	7.7	308	2	Q2YD22_EPTST	Q2yds2 eptaretus
172	251.5	8.0	309	2	Q2YDZ8_EPTST	Q2ydz8 eptaretus	245	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
173	251	8.0	473	1	RTN4R_MOUSE	Q99p18 mus musculus	246	239.5	7.6	307	2	Q2YE04_EPTST	Q2ye04 eptaretus
174	251	8.0	542	2	Q9N4G6_CAEEL	Q9n4g6 caenorhabdi	247	239.5	7.6	370	2	Q8BGX3_MOUSE	Q8bgx3 m adult mal
175	251	8.0	602	2	Q1KS52_PIG	Q1ks52 sus scrofa	248	239.5	7.6	786	2	Q5TU01_ANOGA	Q5tu01 anopheles g
176	251	8.0	622	2	Q72ZQ7_HUMAN	Q72zq7 homo sapien	249	239.5	7.6	1256	2	Q7QCT2_ANOGA	Q7qct2 anopheles g
177	251	8.0	622	2	Q6ZWI5_HUMAN	Q6zwi5 homo sapien	250	238.5	7.6	347	2	Q2YE56_EPTST	Q2ye56 eptaretus



543	207.5	6.6	180	2	0654F0_PETMA	06e4f0 petromyzon	616	203	6.5	602	1	LRC40_MACPA	04r3p6 macaca fasc
544	207.5	6.6	323	2	Q33QT2_EPTST	Q32qt2 eptatretus	617	203	6.5	703	2	Q4SLZ4_TETNG	Q4slz4 tetraodon n
545	207.5	6.6	330	2	Q4S074_TETNG	Q4s074 tetraodon n	618	203	6.5	1514	2	Q9NBK9_DROME	Q9nbk9 drosophila
546	207.5	6.6	518	2	Q62T31_HUMAN	Q62t31 homo sapien	619	203	6.5	1514	2	Q6NN49_DROME	Q6nn49 drosophila
547	207.5	6.6	610	2	Q17GD4_AEAE	Q17gd4 aedes aegyp	620	203	6.5	1514	2	Q9VUN0_DROME	Q9vun0 drosophila
548	207.5	6.6	1329	1	GP124_MOUSE	Q91zv8 mus musculus	621	202.5	6.5	197	2	Q2VGR8_PETMA	Q2vgr8 petromyzon
549	207	6.6	313	1	LRC52_HUMAN	Q8n7c0 homo sapien	622	202.5	6.5	209	2	Q2VGV9_PETMA	Q2vgv9 petromyzon
550	207	6.6	323	2	Q2YE80_EPTBU	Q2ye80 eptatretus	623	202.5	6.5	259	2	Q4GLH5_EPTST	Q4glh5 eptatretus
551	207	6.6	323	2	Q32R43_EPTBU	Q32r43 eptatretus	624	202.5	6.5	259	2	Q4GLK1_EPTST	Q4glk1 eptatretus
552	207	6.6	536	2	Q6P0D2_BRARE	Q6p0d2 brachydanio	625	202.5	6.5	274	2	Q6E4J2_PETMA	Q6e4j2 petromyzon
553	207	6.6	537	2	Q2HPG2_BRARE	Q2hpg2 brachydanio	626	202.5	6.5	322	2	Q32QZ8_EPTBU	Q32qz8 eptatretus
554	207	6.6	613	2	Q50L44_CHICK	Q50l44 gallus gall	627	202.5	6.5	829	2	Q4RIG0_TETNG	Q4rig0 tetraodon n
555	207	6.6	740	1	CT075_HUMAN	Q8wut4 homo sapien	628	202	6.4	271	2	Q4KPI1_LAMAP	Q4kpi1 lampetra ap
556	207	6.6	4293	2	Q08852_MOUSE	Q08852 mus musculus	629	202	6.4	300	2	Q2YE57_EPTST	Q2ye57 eptatretus
557	206.5	6.6	192	2	Q2VGE9_PETMA	Q2vge9 petromyzon	630	202	6.4	321	2	Q32R36_EPTBU	Q32r36 eptatretus
558	206.5	6.6	270	2	Q654K6_PETMA	Q6e4k6 petromyzon	631	202	6.4	321	2	Q32R38_EPTBU	Q32r38 eptatretus
559	206.5	6.6	274	2	Q654C1_PETMA	Q6e4c1 petromyzon	632	202	6.4	324	2	Q32Q58_EPTST	Q32q58 eptatretus
560	206.5	6.6	274	2	Q654B9_PETMA	Q6e4b9 petromyzon	633	202	6.4	1117	2	Q5VQM7_ORYSA	Q5vqm7 oryza sativ
561	206.5	6.6	294	2	Q654L2_PETMA	Q6e4l2 petromyzon	634	202	6.4	1501	2	Q2MIB4_DROPS	Q2mlb4 drosophila
562	206.5	6.6	323	2	Q32Q08_EPTST	Q32q08 eptatretus	635	201.5	6.4	187	2	Q6E4D7_PETMA	Q6e4d7 petromyzon
563	206.5	6.6	327	2	Q5U4S7_XENLA	Q5u4s7 xenopus lae	636	201.5	6.4	275	2	Q4GIJ5_EPTST	Q4gij5 eptatretus
564	206.5	6.6	614	2	Q9D1T0_MOUSE	Q9dit0 mus musculus	637	201.5	6.4	457	2	Q960D1_DROME	Q960d1 drosophila
565	206	6.6	218	2	Q2VGU6_PETMA	Q2vgu6 petromyzon	638	201.5	6.4	524	2	Q4RG59_TETNG	Q4rg59 tetraodon n
566	206	6.6	324	2	Q32QX7_EPTST	Q32qx7 eptatretus	639	201.5	6.4	551	2	Q4RP95_TETNG	Q4rp95 tetraodon n
567	206	6.6	353	1	TSK_HUMAN	Q8wut4 homo sapien	640	201.5	6.4	606	2	Q9BZ20_HUMAN	Q9bz20 homo sapien
568	206	6.6	381	1	PRELP_BOVIN	Q9gkn8 bos taurus	641	201.5	6.4	892	2	P91644_DROME	P91644 drosophila
569	206	6.6	428	2	O14498_HUMAN	Q14498 homo sapien	642	201.5	6.4	1527	2	Q9VZ24_DROME	Q9vz24 drosophila
570	206	6.6	539	2	O5TPW2_ANOGA	Q5tpw2 anopheles g	643	201	6.4	213	2	Q6E4H6_PETMA	Q6e4h6 petromyzon
571	206	6.6	606	2	Q3URE9_MOUSE	Q3ure9 mus musculus	644	201	6.4	218	2	Q6E4K9_PETMA	Q6e4k9 petromyzon
572	206	6.6	606	2	Q8BLC0_MOUSE	Q8blc0 m adult mal	645	201	6.4	322	2	Q32QT1_EPTST	Q32qt1 eptatretus
573	206	6.6	606	2	Q8BZD4_MOUSE	Q8bz4d mus musculus	646	201	6.4	336	2	Q4S8M5_TETNG	Q4s8m5 tetraodon n
574	206	6.6	738	2	Q5UIA7_DROME	Q5uia7 drosophila	647	201	6.4	354	1	TSK_MOUSE	Q8cbr6 mus musculus
575	206	6.6	1054	1	LRIG2_MOUSE	Q52kr2 mus musculus	648	201	6.4	602	1	LRC40_HUMAN	Q9h9a6 homo sapien
576	206	6.6	1127	2	Q4TAT5_TETNG	Q4tat5 tetraodon n	649	201	6.4	712	2	O5BL20_BRARE	O5bl20 brachydanio
577	205.5	6.6	212	2	Q654H2_PETMA	Q6e4h2 petromyzon	650	201	6.4	1391	2	Q29C89_DROPS	Q29c89 drosophila
578	205.5	6.6	479	2	Q6DH76_BRARE	Q6dh76 brachydanio	651	200.5	6.4	845	1	SLIK2_HUMAN	Q9hl56 homo sapien
579	205.5	6.6	492	2	Q99KT6_MOUSE	Q99kt6 mus musculus	652	200.5	6.4	845	1	Q2KHN3_HUMAN	Q2khn3 homo sapien
580	205.5	6.6	590	1	LRTM4_MOUSE	Q80xg9 mus musculus	653	200.5	6.4	845	2	Q2XXV6_DROYA	Q2xxv6 drosophila
581	205	6.5	248	2	Q4G1K4_EPTST	Q4g1k4 eptatretus	654	200.5	6.4	1336	2	Q2XXV7_DROYA	Q2xxv7 drosophila
582	205	6.5	256	2	Q4G1L6_EPTBU	Q4g1l6 eptatretus	655	200.5	6.4	1337	2	Q2XXV7_DROYA	Q2xxv7 drosophila
583	205	6.5	320	2	Q32QR9_EPTST	Q32qr9 eptatretus	656	200	6.4	218	2	Q2VGY1_PETMA	Q2vgy1 petromyzon
584	205	6.5	322	2	Q2YES4_EPTST	Q2yes4 eptatretus	657	200	6.4	280	2	Q2YE26_EPTBU	Q2ye26 eptatretus
585	205	6.5	322	2	Q2YE63_EPTST	Q2ye63 eptatretus	658	200	6.4	460	2	Q4RK03_TETNG	Q4rk03 tetraodon n
586	205	6.5	322	2	Q32Q6_EPTST	Q32q6 eptatretus	659	200	6.4	547	2	Q1EGK1_FUGURIP	Q1egk1 fugu rubrip
587	205	6.5	324	2	Q2VE84_EPTST	Q2ve84 eptatretus	660	200	6.4	616	2	O58A95_CABEL	O58a95 caenorhabdi
588	205	6.5	486	2	Q4RU74_TETNG	Q4ru74 tetraodon n	661	200	6.4	653	2	O23229_CABEL	O23229 caenorhabdi
589	205	6.5	614	2	Q5RDJ4_PONPY	Q5rdj4 pongo pygma	662	199.5	6.4	227	2	Q4SP28_TETNG	Q4sp28 tetraodon n
590	205	6.5	614	2	Q9N008_MACFA	Q9n008 macaca fasc	663	199.5	6.4	261	2	Q4GIL4_EPTBU	Q4gil4 eptatretus
591	205	6.5	620	2	Q96FE5_HUMAN	Q96fe5 homo sapien	664	199.5	6.4	319	2	Q32QN9_EPTST	Q32qn9 eptatretus
592	204.5	6.5	322	2	Q32R03_EPTBU	Q32r03 eptatretus	665	199.5	6.4	622	2	Q66HV9_BRARE	Q66hv9 brachydanio
593	204.5	6.5	323	2	Q32QX2_EPTST	Q32qx2 eptatretus	666	199	6.3	260	2	Q2YE05_EPTST	Q2ye05 eptatretus
594	204.5	6.5	463	2	Q8CLV9_MOUSE	Q8clv9 mus musculus	667	199	6.3	298	2	Q32QM3_EPTST	Q32qm3 eptatretus
595	204	6.5	196	2	Q2VGM9_PETMA	Q2vgm9 petromyzon	668	199	6.3	322	2	Q32QV5_EPTST	Q32qv5 eptatretus
596	204	6.5	276	2	Q2YE25_EPTST	Q2ye25 eptatretus	669	199	6.3	322	2	Q32QV8_EPTST	Q32qv8 eptatretus
597	204	6.5	323	2	Q32R20_EPTBU	Q32r20 eptatretus	670	199	6.3	323	2	Q32R07_EPTBU	Q32r07 eptatretus
598	204	6.5	323	2	Q2VE81_EPTBU	Q2ve81 eptatretus	671	199	6.3	323	2	Q32QY5_EPTBU	Q32qy5 eptatretus
599	204	6.5	353	1	TSK_RAT	Q6gmy6 rattus norv	672	199	6.3	323	2	Q32R24_EPTBU	Q32r24 eptatretus
600	204	6.5	1173	2	Q9V7J8_DROME	Q9v7j8 drosophila	673	199	6.3	324	2	Q32QT9_EPTST	Q32qt9 eptatretus
601	204	6.5	1306	2	Q6P4S1_XENLA	Q6p4s1 xenopus lae	674	199	6.3	846	1	SLIK2_MOUSE	Q8l0c0 mus musculus
602	203.5	6.5	219	2	Q2VGZ2_PETMA	Q2vgz2 petromyzon	675	199	6.3	862	2	Q4SST3_TETNG	Q4sst3 tetraodon n
603	203.5	6.5	299	2	Q32QX3_EPTST	Q32qx3 eptatretus	676	199	6.3	1328	2	Q21043_CABEL	Q21043 caenorhabdi
604	203.5	6.5	845	2	Q6AI13_HUMAN	Q6ai13 homo sapien	677	198.5	6.3	259	2	Q4GLJ4_EPTST	Q4glj4 eptatretus
605	203.5	6.5	894	2	Q9VKG1_DROME	Q9vkg1 drosophila	678	198.5	6.3	320	2	O6YN44_HUMAN	O6yn44 homo sapien
606	203.5	6.5	1061	2	Q5JME4_ORYSA	Q5jme4 oryza sativ	679	198.5	6.3	322	2	Q32R17_EPTBU	Q32r17 eptatretus
607	203.5	6.5	1065	1	LRIG2_HUMAN	Q2vgc8 petromyzon	680	198.5	6.3	548	2	Q1EGL0_PANTR	Q1egh0 pan troglod
608	203	6.5	218	2	Q2VGC8_PETMA	Q2vgc8 petromyzon	681	198.5	6.3	617	1	LRC21_RAT	Q9jmh2 rattus norv
609	203	6.5	269	2	Q654B6_PETMA	Q6e4b6 petromyzon	682	198.5	6.3	741	2	Q4SWG9_TETNG	Q4swg9 tetraodon n
610	203	6.5	286	2	Q2VE17_EPTST	Q2ve17 eptatretus	683	198.5	6.3	873	2	O7XR24_ORYSA	O7xr24 oryza sativ
611	203	6.5	321	2	Q32QZ4_EPTBU	Q32qz4 eptatretus	684	198.5	6.3	1331	1	GP124_HUMAN	Q96pe1 homo sapien
612	203	6.5	323	2	Q32R15_EPTBU	Q32r15 eptatretus	685	198	6.3	192	2	Q2VH08_PETMA	Q2vh08 petromyzon
613	203	6.5	324	2	Q32QR5_EPTST	Q32qr5 eptatretus	686	198	6.3	298	2	Q32QN7_EPTST	Q32qn7 eptatretus
614	203	6.5	324	2	Q2VE71_EPTST	Q2ve71 eptatretus	687	198	6.3	322	2	Q32QP4_EPTST	Q32qp4 eptatretus
615	203	6.5	428	2	Q5NVQ6_PONPY	Q5nvq6 pongo pygma	688	198	6.3	323	2	Q32R16_EPTBU	Q32r16 eptatretus

689	198	6.3	323	2	Q32R22_EPTBU	Q32r22 eptaretus	762	193.5	6.2	545	1	LG12_HUMAN	Q8n0v4 homo sapien
690	198	6.3	324	2	Q32Q08_EPTST	Q32q08 eptaretus	763	193.5	6.2	545	2	Q3MIN2_HUMAN	Q3min2 homo sapien
691	198	6.3	363	2	Q7SYE5_BRARE	Q7sy5e5 brachydanio	764	193.5	6.2	545	2	Q1EGL1_PANTR	Q1egl1 pan troglod
692	198	6.3	602	1	LRC40_PONPY	Q7sy69 pongo pygma	765	193.5	6.2	574	2	Q60W68_CAEBR	Q60w68 caenorhabdi
693	197.5	6.3	193	2	Q2VGP6_PETMA	Q2v6p6 petromyzon	766	193.5	6.2	721	1	Y20B2_MYCTU	Q10690 mycobacteri
694	197.5	6.3	280	2	Q6E4K3_PETMA	Q6e4k3 petromyzon	767	193.5	6.2	721	2	Q7T224_MYCBO	Q7t224 mycobacteri
695	197.5	6.3	300	2	Q6E4K8_PETMA	Q6e4k8 petromyzon	768	193.5	6.2	816	2	Q1KL20_FUGRU	Q1kl20 fugu rubrip
696	197.5	6.3	323	2	Q32Q03_EPTST	Q32q03 eptaretus	769	193.5	6.2	863	2	Q46A62_METBF	Q46a62 methanosarc
697	197.5	6.3	441	2	Q4VBZ3_HUMAN	Q4vbz3 homo sapien	770	193.5	6.2	881	2	Q2XY26_DROME	Q2xy26 drosophila
698	197.5	6.3	437	2	Q9VE49_DROME	Q9ve49 drosophila	771	193.5	6.2	881	2	Q2XY24_DROSI	Q2xy24 drosophila
699	197.5	6.3	548	1	LG13_HUMAN	Q8n145 homo sapien	772	193.5	6.2	910	1	PIDD_HUMAN	Q9hb75 homo sapien
700	197.5	6.3	548	2	Q4RH3_MACFA	Q4r4h3 macaca fasc	773	193.5	6.2	967	2	Q3UVD5_MOUSE	Q3uvd5 mus musculu
701	197.5	6.3	818	2	Q4SIX2_TETNG	Q4s1x2 tetraodon n	774	193.5	6.2	977	1	SLIK3_HUMAN	Q94933 homo sapien
702	197.5	6.3	835	2	Q4SFB0_TETNG	Q4sfb0 tetraodon n	775	193.5	6.2	977	2	Q1RMY6_HUMAN	Q1rmy6 homo sapien
703	197.5	6.3	1321	1	GP125_HUMAN	Q8i1w6 homo sapien	776	193.5	6.2	1333	2	Q2XXV8_DROSI	Q2xxv8 drosophila
704	197	6.3	248	2	Q2YEL6_EPTST	Q2yel6 eptaretus	777	193.5	6.2	1333	2	Q2XXV9_DROSI	Q2xxv9 drosophila
705	197	6.3	320	2	Q32Q09_EPTST	Q32q09 eptaretus	778	193	6.2	252	2	Q4G112_EPTST	Q4g112 eptaretus
706	197	6.3	322	2	Q32Q06_EPTST	Q32q06 eptaretus	779	193	6.2	319	2	Q32R40_EPTBU	Q32r40 eptaretus
707	197	6.3	345	2	Q9HBL6_HUMAN	Q9hb16 homo sapien	780	193	6.2	321	2	Q32R11_EPTBU	Q32r11 eptaretus
708	197	6.3	694	2	Q6YXX5_ORYSA	Q6yxx5 oryza sativ	781	193	6.2	324	2	Q32Q02_EPTST	Q32q02 eptaretus
709	197	6.3	1093	2	Q5XWD3_HUMAN	Q5xwd3 homo sapien	782	193	6.2	497	2	Q4SZU8_TETNG	Q4szu8 tetraodon n
710	196.5	6.3	209	2	Q2VGH6_PETMA	Q2vdh6 petromyzon	783	193	6.2	538	2	Q2LZK6_DROPS	Q2lzk6 drosophila
711	196.5	6.3	259	2	Q4GLJ3_EPTST	Q4glj3 eptaretus	784	193	6.2	545	2	Q2HFF8_BRARE	Q2hpf8 brachydanio
712	196.5	6.3	259	2	Q2YEL2_EPTST	Q2yel2 eptaretus	785	193	6.2	550	2	Q9VJN8_DROME	Q9vjn8 drosophila
713	196.5	6.3	261	2	Q4G1J1_EPTST	Q4g1j1 eptaretus	786	193	6.2	743	2	Q17AC3_AEDAB	Q17ac3 aedes aegyp
714	196.5	6.3	322	2	Q32QY4_EPTBU	Q32qy4 eptaretus	787	192.5	6.1	185	2	Q2VGZ4_PETMA	Q2vgz4 petromyzon
715	196.5	6.3	351	2	Q2L292_DROPS	Q2l292 drosophila	788	192.5	6.1	187	2	Q6E4D5_PETMA	Q6e4d5 petromyzon
716	196.5	6.3	1332	2	Q2XXV5_DROER	Q2xxv5 drosophila	789	192.5	6.1	195	2	Q2VH18_PETMA	Q2vh18 petromyzon
717	196.5	6.3	1333	2	Q2XXW0_DROME	Q2xxw0 drosophila	790	192.5	6.1	214	2	Q6E4G0_PETMA	Q6e4g0 petromyzon
718	196	6.3	263	2	Q6E4D0_PETMA	Q6e4d0 petromyzon	791	192.5	6.1	259	2	Q4G1H7_EPTST	Q4g1h7 eptaretus
719	196	6.3	300	2	Q32QX6_EPTST	Q32qx6 eptaretus	792	192.5	6.1	299	2	Q32QV1_EPTST	Q32qv1 eptaretus
720	196	6.3	3638	2	Q15142_HUMAN	Q15142 homo sapien	793	192.5	6.1	322	2	Q32QY3_EPTBU	Q32qy3 eptaretus
721	195.5	6.2	274	2	Q1EGJ6_CHICK	Q1egj6 gallus gall	794	192.5	6.1	438	2	Q6GU68_MOUSE	Q6gu68 mus musculu
722	195.5	6.2	288	2	Q32G76_EPTBU	Q32g76 eptaretus	795	192.5	6.1	542	2	Q50BZ7_MOUSE	Q50bd7 mus musculu
723	195.5	6.2	323	2	Q2YB59_EPTST	Q2yeb59 eptaretus	796	192.5	6.1	575	2	Q23580_CAEEL	Q23580 caenorhabdi
724	195.5	6.2	370	2	Q58D17_BOVIN	Q58d17 bos taurus	797	192.5	6.1	887	2	Q2XY21_DROER	Q2xy21 drosophila
725	195.5	6.2	378	1	PRELP_MOUSE	Q9jk53 mus musculu	798	192.5	6.1	887	2	Q6HA06_CRAGI	Q6ha06 crassostrea
726	195.5	6.2	378	2	Q543S0_MOUSE	Q543s0 mus musculu	799	192.5	6.1	1093	2	Q6E4K2_PETMA	Q6e4k2 petromyzon
727	195.5	6.2	543	2	Q29K00_DROPS	Q29k00 drosophila	800	192	6.1	265	2	Q6E4C5_PETMA	Q6e4c5 petromyzon
728	195.5	6.2	917	2	Q86PM1_DROME	Q86pm1 drosophila	801	192	6.1	273	2	Q6E4C5_PETMA	Q6e4c5 petromyzon
729	195.5	6.2	931	2	Q9VMW16_DROME	Q9vmw16 drosophila	802	192	6.1	300	2	Q2YB86_EPTST	Q2yeb86 eptaretus
730	195	6.2	322	2	Q32Q09_EPTST	Q32q09 eptaretus	803	192	6.1	548	1	LG13_MOUSE	Q8k406 mus musculu
731	195	6.2	440	2	Q4RSH2_MACFA	Q4rsh2 macaca fasc	804	192	6.1	548	2	Q3V1R3_MOUSE	Q3v1r3 mus musculu
732	195	6.2	526	2	Q1EGJ8_CHICK	Q1egj8 gallus gall	805	192	6.1	627	2	Q6UN14_LEICH	Q6un14 leishmania
733	195	6.2	614	2	Q6NUK3_HUMAN	Q6nuk3 homo sapien	806	191.5	6.1	185	2	Q2VGS8_PETMA	Q2vgs8 petromyzon
734	195	6.2	620	2	Q6XUM3_HUMAN	Q6xum3 homo sapien	807	191.5	6.1	187	2	Q6E4I7_PETMA	Q6e4i7 petromyzon
735	195	6.2	837	1	SLIK4_HUMAN	Q8i1w52 homo sapien	808	191.5	6.1	193	2	Q2VGT8_PETMA	Q2vgt8 petromyzon
736	195	6.2	837	2	Q29DD0_DROPS	Q29dd0 drosophila	809	191.5	6.1	204	2	Q6E4J8_PETMA	Q6e4j8 petromyzon
737	195	6.2	1536	2	Q2YB82_EPTBU	Q2yeb82 eptaretus	810	191.5	6.1	915	1	PIDD_MOUSE	Q9erv7 mus musculu
738	194.5	6.2	322	2	Q32QV9_EPTST	Q32qv9 eptaretus	811	191.5	6.1	980	1	SLIK3_MOUSE	Q810b9 mus musculu
739	194.5	6.2	323	2	TSK_CHICK	Q65291 gallus gall	812	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nzm5 mus musculu
740	194.5	6.2	369	1	Q3MHH9_BOVIN	Q3mhh9 bos taurus	813	191	6.1	192	2	Q2VGN8_PETMA	Q2vgn8 petromyzon
741	194.5	6.2	680	2	Q7Z3D0_HUMAN	Q7z3d0 homo sapien	814	191	6.1	194	2	Q2VGE8_PETMA	Q2vge8 petromyzon
742	194.5	6.2	693	2	ECM2_HUMAN	Q94769 homo sapien	815	191	6.1	271	2	Q4KP00_LAMAP	Q4kp00 lampetra ap
743	194.5	6.2	699	1	Q5T9F2_HUMAN	Q5t9f2 homo sapien	816	191	6.1	440	2	Q5RCQ8_PONPY	Q5rcq8 pongo pygma
744	194.5	6.2	699	2	Q96SM3_CAEEL	Q96sm3 caenorhabdi	817	191	6.1	456	2	Q28XA4_DROPS	Q28xa4 drosophila
745	194.5	6.2	737	2	Q96SM2_CAEEL	Q96sm2 caenorhabdi	818	191	6.1	536	2	Q173K1_AEDAE	Q173k1 aedes aegyp
746	194.5	6.2	881	2	Q96SM2_CAEEL	Q96sm2 caenorhabdi	819	191	6.1	610	2	Q4TLM0_TETNG	Q4tlm0 tetraodon n
747	194.5	6.2	1630	1	LAP4_HUMAN	Q14160 homo sapien	820	191	6.1	757	2	Q28XQ2_DROPS	Q28xq2 drosophila
748	194	6.2	192	2	Q2VGL7_PETMA	Q2vgj7 petromyzon	821	191	6.1	868	2	Q2XQ10_CHICK	Q2xq10 gallus gall
749	194	6.2	258	2	Q4G1J0_EPTST	Q4g1j0 eptaretus	822	191	6.1	251	2	Q4G117_EPTST	Q4g117 eptaretus
750	194	6.2	258	2	Q4G110_EPTST	Q4g110 eptaretus	823	190.5	6.1	536	2	Q2HPC1_BRARE	Q2hpg1 brachydanio
751	194	6.2	263	2	Q6E4C0_PETMA	Q6e4c0 petromyzon	824	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721 fugu rubrip
752	194	6.2	320	2	Q32Q03_EPTST	Q32q03 eptaretus	825	190.5	6.1	1238	2	Q6NR19_DROME	Q6nr19 drosophila
753	194	6.2	611	2	Q4RHK3_TETNG	Q4rhk3 tetraodon n	826	190.5	6.1	1343	2	Q17NJ1_AEDAE	Q17nj1 aedes aegyp
754	194	6.2	692	2	Q4RV46_TETNG	Q4rv46 tetraodon n	827	190.5	6.1	1535	2	Q9VPF0_DROME	Q9vpf0 drosophila
755	194	6.2	836	2	Q9V9V6_DROME	Q9v9v6 drosophila	828	190	6.1	191	2	Q6E4H3_PETMA	Q6e4h3 petromyzon
756	193.5	6.2	186	2	Q6E4H8_PETMA	Q6e4h8 petromyzon	829	190	6.1	536	2	Q16P99_AEDAE	Q16p99 aedes aegyp
757	193.5	6.2	270	2	Q4KP03_LAMAP	Q4kp03 lampetra ap	830	190	6.1	639	2	Q4RE68_TETNG	Q4re68 tetraodon n
758	193.5	6.2	273	2	Q4GLM1_EPTBU	Q4glm1 eptaretus	831	190	6.1	654	2	Q628N6_CAEBR	Q628n6 caenorhabdi
759	193.5	6.2	377	1	PRELP_RAT	Q9eqp5 rattus norv	832	190	6.1	733	1	CT075_MOUSE	P59383 mus musculu
760	193.5	6.2	378	2	Q8CAZ3_MOUSE	Q8cacz3 mus musculu	833	190	6.1	1119	1	LRIG3_HUMAN	Q6uxm1 homo sapien
	193.5	6.2	433	2	Q6E4H8_PETMA	Q6e4h8 petromyzon	834	190	6.1	1346	2	Q9V477_DROME	Q9v477 drosophila

835	190	6.1	2800	2	Q6XHB1_DICTDI	Q6xbh1 dictyosteli	908	185.5	5.9	185	2	Q2VGV1_PETMA	Q2vGV1 petromyzon
836	190	6.1	2800	2	Q1ZXD6_DICTDI	Q1zxd6 dictyosteli	909	185.5	5.9	191	2	Q2VGC6_PETMA	Q2vGC6 petromyzon
837	189.5	6.0	252	2	Q4G1J7_DICTST	Q4g1j7 dictatretus	910	185.5	5.9	191	2	Q2VGR0_PETMA	Q2vGR0 petromyzon
838	189.5	6.0	370	2	Q4RSX9_TETNG	Q4rsx9 tetraodon n	911	185.5	5.9	191	2	Q2VGT6_PETMA	Q2vGT6 petromyzon
839	189.5	6.0	880	2	Q2XY23_DROYA	Q2xy23 drosophila	912	185.5	5.9	195	2	Q2VGR6_PETMA	Q2vGR6 petromyzon
840	189	6.0	192	2	Q2VGP2_PETMA	Q2vgp2 petromyzon	913	185.5	5.9	251	2	Q2YE24_EPTST	Q2ye24 eptatretus
841	189	6.0	298	2	Q3Q0U2_EPTST	Q3q0u2 eptatretus	914	185.5	5.9	369	2	Q4T3M1_TETNG	Q4t3m1 tetraodon n
842	189	6.0	369	1	PGS1_MOUSE	P28653 mus musculus	915	185.5	5.9	466	2	Q661W3_XENLA	Q661w3 xenopus lae
843	189	6.0	369	1	PGS1_RAT	P28653 rattus norv	916	185.5	5.9	795	2	Q297R4_DROPS	Q297r4 drosophila
844	189	6.0	369	1	Q3TNY9_MOUSE	Q3tny9 m 15 days e	917	185.5	5.9	953	2	Q6MF87_PARUM	Q6mf87 parachlamyd
845	189	6.0	627	2	Q4T5R5_TETNG	Q4t5r5 tetraodon n	918	185	5.9	254	2	Q4S4N7_TETNG	Q4s4n7 tetraodon n
846	189	6.0	760	2	Q4QI81_LEIMA	Q4q818 leishmania	919	185	5.9	333	2	Q32R21_EPTBU	Q32r21 eptatretus
847	189	6.0	839	2	Q9SN46_ARATH	Q9sn46 arabidopsis	920	185	5.9	389	2	Q6BP5_ERARE	Q6bp5 brachydanio
848	189	6.0	1392	2	Q9VAD1_DROME	Q9vad1 drosophila	921	185	5.9	512	2	Q6PEZ8_HUMAN	Q6pez8 homo sapien
849	189	6.0	4311	2	Q7YOK5_CANFA	Q7yok5 canis famill	922	185	5.9	603	1	LRC40_CHICK	Q521n0 gallus gall
850	188.5	6.0	348	2	Q3QV7_EPTST	Q3qv7 eptatretus	923	184.5	5.9	257	2	Q4G1L5_EPTBU	Q4g1l5 eptatretus
851	188.5	6.0	369	2	Q6GM15_ERARE	Q6gm15 brachydanio	924	184.5	5.9	259	2	Q2YE09_EPTST	Q2ye09 eptatretus
852	188.5	6.0	370	2	Q1LXA7_ERARE	Q1lxa7 brachydanio	925	184.5	5.9	270	2	Q4KP09_LAMAP	Q4kp09 lampetra ap
853	188.5	6.0	370	2	Q504E0_BRARE	Q504e0 brachydanio	926	184.5	5.9	608	2	Q17FY2_AEDAE	Q17fy2 aedes aegyp
854	188.5	6.0	410	2	Q9DDZ7_PETMA	Q9ddz7 petromyzon	927	184.5	5.9	724	2	Q5XWB9_HORSE	Q5xwb9 equus cabal
855	188.5	6.0	433	2	Q5SVH5_MOUSE	Q5svh5 mus musculus	928	184.5	5.9	799	2	Q9V964_DROME	Q9v964 drosophila
856	188.5	6.0	440	1	OMGP_MOUSE	Q63912 mus musculus	929	184.5	5.9	839	2	Q692V6_MOUSE	Q692v6 mus musculus
857	188.5	6.0	440	2	Q3UVU3_MOUSE	Q3uvu3 mus musculus	930	184.5	5.9	841	2	Q5F4K7_PIG	Q5f4k7 sus scrofa
858	188.5	6.0	538	2	Q5Z8W0_ORYSA	Q5z8w0 oryza sativ	931	184.5	5.9	841	2	Q2TNK4_PIG	Q2tnk4 sus scrofa
859	188.5	6.0	555	2	Q4SBU9_TETNG	Q4sbu9 tetraodon n	932	184.5	5.9	843	1	TLR4_HORSE	Q9myk3 equus cabal
860	188.5	6.0	677	2	Q3KR19_HUMAN	Q3kr19 homo sapien	933	184.5	5.9	957	1	SLIK5_MOUSE	Q810b7 mus musculus
861	188	6.0	218	2	Q2VGY9_PETMA	Q2vgy9 petromyzon	934	184.5	5.9	1007	2	Q6XSX3_ORYSA	Q65xs3 oryza sativ
862	188	6.0	324	2	Q32OR1_EPTST	Q32or1 eptatretus	935	184.5	5.9	1046	2	Q5G097_CHICK	Q5g097 gallus gall
863	188	6.0	368	2	Q53HU6_HUMAN	Q53hu6 homo sapien	936	184.5	5.9	1214	2	Q69JN6_ORYSA	Q69jn6 oryza sativ
864	188	6.0	369	1	PGS1_CANFA	Q02678 mus musculus	937	184	5.9	187	2	Q6E4M5_PETMA	Q6e4m5 petromyzon
865	188	6.0	369	2	Q3UXK8_MOUSE	Q3uxk8 mus musculus	938	184	5.9	192	2	Q2VGJ6_PETMA	Q2vgj6 petromyzon
866	188	6.0	369	2	Q7TWM3_MOUSE	Q7twm3 mus musculus	939	184	5.9	253	2	Q6E4K5_PETMA	Q6e4k5 petromyzon
867	188	6.0	522	1	LRTM1_MOUSE	Q8k377 mus musculus	940	184	5.9	263	2	Q6E4K7_PETMA	Q6e4k7 petromyzon
868	188	6.0	626	2	Q4SE92_TETNG	Q4se92 tetraodon n	941	184	5.9	274	2	Q4G1M0_EPTBU	Q4g1m0 eptatretus
869	188	6.0	818	2	Q5Z1H8_CHICK	Q5zin8 gallus gall	942	184	5.9	291	2	Q4RF21_TETNG	Q4rf21 tetraodon n
870	187.5	6.0	195	2	Q2VGR5_PETMA	Q2vgr5 petromyzon	943	184	5.9	368	1	PGS1_HUMAN	P21810 homo sapien
871	187.5	6.0	259	2	Q4G1L0_EPTBU	Q4g1l0 eptatretus	944	184	5.9	368	2	Q53F14_HUMAN	Q53f14 homo sapien
872	187.5	6.0	310	2	Q9DDZ8_PETMA	Q9ddz8 petromyzon	945	184	5.9	369	2	Q3TAF9_MOUSE	Q3taf9 mus musculus
873	187.5	6.0	350	1	TSK_XENTR	Q9d4z8 xenopus tro	946	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g
874	187.5	6.0	363	2	Q9H5G9_HUMAN	Q9h5g9 homo sapien	947	184	5.9	543	2	Q4RC6_TETNG	Q4rgc6 tetraodon n
875	187.5	6.0	425	2	Q9VGH2_DROME	Q9vgh2 drosophila	948	184	5.9	552	2	Q6KX6_ORYSA	Q6kx6 oryza sativ
876	187.5	6.0	601	1	LRC40_BRARE	Q7swx3 brachydanio	949	184	5.9	565	2	Q7PJD0_ANOGA	Q7pjd0 anopheles g
877	187.5	6.0	861	2	Q4ZJ82_CHICK	Q4zj82 gallus gall	950	184	5.9	837	1	SLIK4_MOUSE	Q810b8 mus musculus
878	187.5	6.0	885	2	Q2XY22_DROYA	Q2xy22 drosophila	951	184	5.9	1058	2	Q3MNF2_BOVIN	Q3mnf2 bos taurus
879	187	6.0	260	2	Q4G1K7_EPTST	Q4g1k7 eptatretus	952	183.5	5.9	187	2	Q6E4F6_PETMA	Q6e4f6 petromyzon
880	187	6.0	262	2	Q4G1K0_EPTST	Q4g1k0 eptatretus	953	183.5	5.9	287	2	Q6WZB9_DROME	Q6wzb9 drosophila
881	187	6.0	324	2	Q2YE79_EPTST	Q2ye79 eptatretus	954	183.5	5.9	292	2	Q6NYI6_DROME	Q6nyy6 brachydanio
882	187	6.0	592	2	Q61PG4_CABBR	Q61pg4 caenorhabdi	955	183.5	5.9	652	2	Q7Q696_ANOGA	Q7q696 anopheles g
883	187	6.0	615	2	Q9VZ84_DROME	Q9vz84 drosophila	956	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus
884	187	6.0	735	2	Q6E114_MOUSE	Q6e114 mus musculus	957	183.5	5.9	795	1	TLR1_MOUSE	Q9epg1 mus musculus
885	187	6.0	807	2	Q16TW7_AEDAE	Q16tw7 aedes aegyp	958	183.5	5.9	824	2	Q5GXX1_PIG	Q5gxx1 sus scrofa
886	187	6.0	818	2	Q5WA51_CHICK	Q5wa51 gallus gall	959	183.5	5.9	841	1	TLR4_PIG	Q6y956 sus scrofa
887	187	6.0	1741	2	Q5LJU2_DROME	Q5lj02 drosophila	960	183.5	5.9	841	2	Q401C7_PIG	Q401c7 sus scrofa
888	186.5	5.9	193	2	Q2VHC4_PETMA	Q2vhc4 petromyzon	961	183.5	5.9	864	2	Q2XY30_DROSI	Q2xy30 drosophila
889	186.5	5.9	323	2	Q3QV0_EPTST	Q3qv0 eptatretus	962	183.5	5.9	864	2	Q2XY31_DROSI	Q2xy31 drosophila
890	186.5	5.9	368	1	PGS1_XENLA	Q9ib75 xenopus lae	963	183.5	5.9	867	2	Q2XY27_DROER	Q2xy27 drosophila
891	186.5	5.9	521	2	Q7ZU34_LEPIC	Q7zu34 leptospira	964	183.5	5.9	871	2	Q2XY28_DROYA	Q2xy28 drosophila
892	186.5	5.9	536	2	Q1EGJ9_FUGRU	Q1egj9 fugu rubrip	965	183.5	5.9	871	2	Q2XY29_DROYA	Q2xy29 drosophila
893	186.5	5.9	639	2	Q5VZ17_HUMAN	Q5vz17 homo sapien	966	183.5	5.9	1059	2	Q5ZJD0_CHICK	Q5zjd0 gallus gall
894	186.5	5.9	799	2	Q5VZ18_HUMAN	Q5vz18 homo sapien	967	183.5	5.9	1322	2	Q2M1B0_DROPS	Q2m1b0 drosophila
895	186.5	5.9	839	1	TLR4_HUMAN	Q00206 homo sapien	968	183.5	5.9	1537	1	LRRC7_HUMAN	Q96nw7 homo sapien
896	186.5	5.9	839	1	TLR4_PANPA	Q9trn0 pan paniscu	969	183	5.8	432	2	Q8BJ09_MOUSE	Q8bj09 mus musculus
897	186.5	5.9	839	2	Q5VZ19_HUMAN	Q5vz19 homo sapien	970	183	5.8	540	2	Q9VU53_DROME	Q9vub3 drosophila
898	186	5.9	216	2	Q2VGS1_PETMA	Q2vgs1 petromyzon	971	183	5.8	568	2	Q6P3Y9_MOUSE	Q6p3y9 mus musculus
899	186	5.9	218	2	Q2VGR4_PETMA	Q2vgr4 petromyzon	972	183	5.8	662	1	LRC32_HUMAN	Q14392 homo sapien
900	186	5.9	273	2	Q6B4B4_PETMA	Q6eb44 petromyzon	973	183	5.8	664	2	Q7ZT81_ONCMY	Q7zt81 oncorhynch
901	186	5.9	368	2	Q5RAY4_PONPY	Q5ray4 pongo pygma	974	183	5.8	673	2	Q17GD6_AEDAE	Q17gd6 aedes aegyp
902	186	5.9	440	1	OMGP_HUMAN	P23515 homo sapien	975	183	5.8	972	2	Q5ZJ34_CHICK	Q5zj34 gallus gall
903	186	5.9	440	2	Q5JHB8_HUMAN	Q5jhb8 homo sapien	976	182.5	5.8	187	2	Q6E4G7_PETMA	Q6e4g7 petromyzon
904	186	5.9	517	2	Q299N9_DROPS	Q299n9 drosophila	977	182.5	5.8	187	2	Q6E4G1_PETMA	Q6e4g1 petromyzon
905	186	5.9	552	2	Q9VT44_DROME	Q9vt44 drosophila	978	182.5	5.8	219	2	Q2VGV7_PETMA	Q2vgv7 petromyzon
906	186	5.9	623	1	LRC21_HUMAN	Q9p2v4 homo sapien	979	182.5	5.8	257	2	Q4G1L8_EPTBU	Q4g1l8 eptatretus
907	186	5.9	1029	1	TLR9_BOVIN	Q5i2m5 bos taurus	980	182.5	5.8	261	2	Q2YE27_EPTBU	Q2ye27 eptatretus

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981	182.5	5.8	298	2	Q320Y7_EPTBU	Q32qy7	eptatretus	1054	179.5	5.7	585	2	Q61GX3_CABER	Q61gx3	caenorhabdi
982	182.5	5.8	379	1	ASPN_HUMAN	Q9bxf1	homo sapien	1055	179.5	5.7	799	2	Q3BBY2_MACMU	Q3bby2	macaca mula
983	182.5	5.8	380	2	Q5TBF3_HUMAN	Q5tbf3	homo sapien	1056	179.5	5.7	820	2	Q5R3F8_HUMAN	Q5r3f8	homo sapien
984	182.5	5.8	384	2	Q6P528_HUMAN	Q6p528	homo sapien	1057	179.5	5.7	1117	1	LRIG3_MOUSE	Q6pvc6	mus musculus
985	182.5	5.8	618	2	Q1L8W7_BRARE	Q1l8w7	brachydanio	1058	179.5	5.7	4283	2	Q9ERV0_RAT	Q9erv0	rattus norv
986	182.5	5.8	810	2	Q8T3J2_DROME	Q8t3j2	drosophila	1059	179.5	5.7	192	2	Q2VH01_PETMA	Q2vh01	petromyzon
987	182.5	5.8	811	2	Q9VK54_DROME	Q9vk54	drosophila	1060	179.5	5.7	192	2	Q2VGC7_PETMA	Q2vgc7	petromyzon
988	182.5	5.8	828	1	TLR4_PONPY	Q8spe8	pongo pygma	1061	179.5	5.7	192	2	Q2VGV8_PETMA	Q2vgv8	petromyzon
989	182.5	5.8	837	1	TLR4_GORGO	Q8spe8	gorilla gor	1062	179.5	5.7	194	2	Q2VH46_PETMA	Q2vh46	petromyzon
990	182.5	5.8	864	2	Q2XV32_DROME	Q2xy32	drosophila	1063	179.5	5.7	262	2	Q2VE11_EPTST	Q2ve11	eptatretus
991	182.5	5.8	880	2	P91643_DROME	P91643	drosophila	1064	179.5	5.7	273	2	Q6E4B8_PETMA	Q6eb48	petromyzon
992	182.5	5.8	958	1	SLIK5_HUMAN	Q49991	homo sapien	1065	179.5	5.7	314	1	LRCS52_MOUSE	Q5m8m9	mus musculus
993	182.5	5.8	958	2	Q5V781_HUMAN	Q5v781	homo sapien	1066	179.5	5.7	534	2	Q9VT89_DROME	Q9vt89	drosophila
994	182.5	5.8	958	2	Q4QOH1_HUMAN	Q4qoh1	homo sapien	1067	179.5	5.7	700	2	Q9P244_HUMAN	Q9p244	homo sapien
995	182.5	5.8	999	2	Q17PVO_AEDAE	Q17pv0	aedes aegyp	1068	179.5	5.7	742	2	Q9BJD4_STRPU	Q9bjd4	strongyloce
996	182.5	5.8	1041	2	Q3HJ14_TRIER	Q3hj14	trichodesmi	1069	179.5	5.7	815	1	Q17LD1_AEDAE	Q17ld1	aedes aegyp
997	182.5	5.8	192	2	Q2VGF9_PETMA	Q2vgf9	petromyzon	1070	179.5	5.7	905	1	TLR3_MOUSE	Q99mb1	mus musculus
998	182.5	5.8	194	2	Q2VGZ0_PETMA	Q2vgz0	petromyzon	1071	179.5	5.7	905	2	Q499F3_MOUSE	Q499f3	mus musculus
999	182.5	5.8	205	2	Q4R9X7_TETNG	Q4r9x7	tetraodon n	1072	179.5	5.7	969	2	Q4LBC9_ONCMY	Q4lbc9	oncorhynchus
1000	182.5	5.8	252	2	Q4GI18_EPTST	Q4gi18	eptatretus	1073	179.5	5.7	1029	1	TLR9_SHEEP	Q512m4	ovis aries
1001	182.5	5.8	271	2	Q6E4C4_PETMA	Q6e4c4	petromyzon	1074	178.5	5.7	161	2	Q2VH51_PETMA	Q2vh51	petromyzon
1002	182.5	5.8	297	2	Q4RU73_TETNG	Q4ru73	tetraodon n	1075	178.5	5.7	176	2	Q567L5_BRARE	Q567l5	brachydanio
1003	182.5	5.8	319	2	Q32R34_EPTBU	Q32r34	eptatretus	1076	178.5	5.7	190	2	Q6E4D8_PETMA	Q6e4d8	petromyzon
1004	182.5	5.8	369	1	PGS1_BOVIN	F21809	bos taurus	1077	178.5	5.7	348	2	Q5RI43_BRARE	Q5ri43	brachydanio
1005	182.5	5.8	369	1	PGS1_SHEEP	Q46390	ovis aries	1078	178.5	5.7	356	1	PGS2_COTJA	Q9de68	coturnix co
1006	182.5	5.8	369	2	Q17QB0_BOVIN	Q17qb0	bos taurus	1079	178.5	5.7	443	1	AMG01_HUMAN	Q67vv7	oryza sativ
1007	182.5	5.8	373	2	Q5RI45_BRARE	Q5ri45	brachydanio	1080	178.5	5.7	493	1	Q4OGJ5_LEIMA	Q4ogj5	leishmania
1008	182.5	5.8	373	2	Q803T1_BRARE	Q803t1	brachydanio	1081	178.5	5.7	587	2	POPC_RALSO	Q4qg19	leishmania
1009	182.5	5.8	428	2	Q8P3F8_LEPIN	Q8p3f8	leptosira	1082	178.5	5.7	1024	1	POPC_RALSO	Q9rb22	ralstonia s
1010	182.5	5.8	532	2	Q96671_DROSOPHILA	Q96671	drosophila	1083	178.5	5.7	1063	2	Q5Z666_ORYSA	Q5z666	oryza sativ
1011	182.5	5.8	678	2	Q8HXV0_BOVIN	Q8hxv0	bos taurus	1084	178.5	5.7	1104	2	Q7XUH4_ORYSA	Q7xuh4	oryza sativ
1012	182.5	5.8	1022	2	Q8HXV0_BOVIN	Q8hxv0	bos taurus	1085	178.5	5.7	1107	2	Q3MD20_ANAVT	Q3md20	anabaena va
1013	182.5	5.8	1029	2	Q866B2_BOVIN	Q866b2	bos taurus	1086	178.5	5.7	1310	1	GP125_MOUSE	Q7tt36	mus musculus
1014	181.5	5.8	180	2	Q8BPJ0_MOUSE	Q8bpj0	mus musculus	1087	178.5	5.7	187	2	Q6E4H4_PETMA	Q6e4h4	petromyzon
1015	181.5	5.8	185	2	Q2VGZ9_PETMA	Q2vgz9	petromyzon	1088	178.5	5.7	192	2	Q2VH53_PETMA	Q2vh53	petromyzon
1016	181.5	5.8	191	2	Q2VH42_PETMA	Q2vh42	petromyzon	1089	178.5	5.7	192	2	Q2VH56_PETMA	Q2vh56	petromyzon
1017	181.5	5.8	251	1	Q4G1K2_EPTST	Q4g1k2	eptatretus	1090	178.5	5.7	194	2	Q2VGE4_PETMA	Q2vge4	petromyzon
1018	181.5	5.8	259	2	Q4GIJ8_EPTST	Q4gi18	eptatretus	1091	178.5	5.7	231	2	Q3TV01_MOUSE	Q3tv01	mus musculus
1019	181.5	5.8	298	2	Q32R41_EPTBU	Q32r41	eptatretus	1092	178.5	5.7	296	2	Q32QX9_EPTST	Q32qx9	eptatretus
1020	181.5	5.8	357	1	PGS3_CHICK	F28675	gallus gall	1093	178.5	5.7	298	2	Q32QX4_EPTST	Q32qx4	eptatretus
1021	181.5	5.8	599	2	Q7T3H6_BRARE	Q7t3h6	brachydanio	1094	178.5	5.7	319	2	Q32QZ3_EPTBU	Q32qz3	eptatretus
1022	181.5	5.8	670	2	Q16P50_AEDAE	Q16p50	aedes aegyp	1095	178.5	5.7	364	2	Q6GJ59_XENLA	Q6gj59	xenopus lae
1023	181.5	5.8	699	2	Q61PG3_CABER	Q61pg3	caenorhabdi	1096	178.5	5.7	391	2	Q4RQ11_TETNG	Q4rq11	tetraodon n
1024	181.5	5.8	1434	2	Q17NJ6_AEDAE	Q17nj6	aedes aegyp	1097	178.5	5.7	488	2	Q4RX05_TETNG	Q4rx05	tetraodon n
1025	181.5	5.8	2160	2	Q13488_MAGGR	Q13488	magnaporthie	1098	178.5	5.7	522	1	LRTM1_HUMAN	Q86us6	homo sapien
1026	181.5	5.8	2160	2	Q13328_MAGGR	Q13328	magnaporthie	1099	178.5	5.7	578	2	Q28CE3_XENTR	Q28ce3	xenopus tro
1027	181.5	5.8	192	2	Q2VGY4_PETMA	Q2vgy4	petromyzon	1100	178.5	5.7	894	2	Q9BJD6_STRPU	Q9bjd6	strongyloce
1028	181.5	5.8	298	2	Q2YB69_EPTST	Q2yeb9	eptatretus	1101	178.5	5.7	1049	1	TLR7_HUMAN	Q9nyk1	homo sapien
1029	181.5	5.8	372	1	PGS1_HORSE	Q46403	equus cabal	1102	178.5	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4	homo sapien
1030	181.5	5.8	569	2	Q7QIP3_ANOGA	Q7qip3	anopheles g	1103	178.5	5.7	1257	2	Q7PNF8_ANOGA	Q7pnf8	anopheles g
1031	181.5	5.8	1013	2	Q8LQ10_ORYSA	Q8lq10	oryza sativ	1104	177.5	5.7	187	2	Q2VH41_PETMA	Q2vh41	petromyzon
1032	181.5	5.8	1333	2	Q7Q168_ANOGA	Q7q168	anopheles g	1105	177.5	5.7	195	2	Q2VGD7_PETMA	Q2vgd7	petromyzon
1033	180.5	5.8	371	2	Q6GLQ6_XENLA	Q6glq6	xenopus lae	1106	177.5	5.7	215	2	Q2VGS6_PETMA	Q2vgs6	petromyzon
1034	180.5	5.8	385	2	Q8BWM6_MOUSE	Q8bwm6	mus musculus	1107	177.5	5.7	275	2	Q4G1K5_EPTST	Q4g1k5	eptatretus
1035	180.5	5.8	441	2	Q8I170_DROVI	Q8i170	drosophila	1108	177.5	5.7	796	2	Q4LDR7_PIG	Q4ldr7	sus scrofa
1036	180.5	5.8	522	1	AMG02_PONPY	Q5r7m3	pongo pygma	1109	177.5	5.7	796	2	Q59H19_PIG	Q59h19	sus scrofa
1037	180.5	5.8	584	2	Q6PGX3_BRARE	Q6pgx3	brachydanio	1110	177.5	5.7	809	2	Q4RMQ1_TETNG	Q4rmq1	tetraodon n
1038	180.5	5.8	821	2	Q96PY3_HUMAN	Q96py3	homo sapien	1111	177.5	5.7	1026	2	Q5SMW2_ORYSA	Q5smw2	oryza sativ
1039	180.5	5.8	859	2	Q12ZX0_MUSMM	Q12zx0	mus musculus	1112	177.5	5.7	1050	1	TLR7_MOUSE	Q58681	mus musculus
1040	180.5	5.8	1376	2	Q16X81_AEDAE	Q16x81	aedes aegyp	1113	177.5	5.7	1050	2	Q54870_MOUSE	Q54870	m toll-like
1041	180.5	5.8	1443	2	Q9VJQ0_DROME	Q9vjq0	drosophila	1114	177.5	5.7	1360	2	Q7KTA0_DROME	Q7kta0	drosophila
1042	180.5	5.8	1460	2	Q5H261_XENTR	Q5h261	xenopus tro	1115	177.5	5.7	2300	1	CYAA_NEUCR	Q01631	neuropora
1043	180.5	5.7	192	2	Q2VH29_PETMA	Q2vh29	petromyzon	1116	177.5	5.7	2493	1	CYAA_USIMA	P49606	ustilago ma
1044	180.5	5.7	250	2	Q4G1M2_EPTBU	Q4g1m2	eptatretus	1117	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1	ustilago ma
1045	180.5	5.7	436	2	Q29FB4_DROPS	Q29fb4	drosophila	1118	177.5	5.6	187	2	Q6E4H5_PETMA	Q6e4h5	petromyzon
1046	180.5	5.7	522	1	LRTM1_PONPY	Q5r6b1	pongo pygma	1119	177.5	5.6	192	2	Q2VH26_PETMA	Q2vh26	petromyzon
1047	180.5	5.7	817	2	Q9VS84_DROME	Q9vs84	drosophila	1120	177.5	5.6	192	2	Q2VGQ0_PETMA	Q2vgq0	petromyzon
1048	180.5	5.7	877	2	Q86P15_DROME	Q86p15	drosophila	1121	177.5	5.6	192	2	Q2VGR6_PETMA	Q2vgr6	petromyzon
1049	180.5	5.7	843	2	Q7ZTG5_CHICK	Q7ztg5	gallus gall	1122	177.5	5.6	192	2	Q2VGR2_PETMA	Q2vgr2	petromyzon
1050	180.5	5.7	869	2	Q4S0C1_TETNG	Q4s0c1	tetraodon n	1123	177.5	5.6	192	2	Q2VH28_PETMA	Q2vh28	petromyzon
1051	179.5	5.7	185	2	Q2VG17_PETMA	Q2vg17	petromyzon	1124	177.5	5.6	334	2	Q4SBUS_TETNG	Q4sbu8	tetraodon n
1052	179.5	5.7	187	2	Q6E4D6_PETMA	Q6e4d6	petromyzon	1125	177.5	5.6	343	1	LUM_COTJA	Q9de67	coturnix co
1053	179.5	5.7	195	2	Q2VGP4_PETMA	Q2vgp4	petromyzon	1126	177.5	5.6	615	2	Q29EA2_DROPS	Q29ea2	drosophila

1127	177	5.6	662	1	LRC32_PONPY	Q5xf01	pongo pygma	1200	174	5.6	651	2	Q4JQ02_XENLA	Q4jgq2	xenopus lae
1128	177	5.6	666	2	Q7Q2W6_ANOGA	Q7q2w6	anopheles g	1201	174	5.6	859	1	TLR3_MOUSE	Q9jfi7	mus musculus
1129	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85	m extracell	1202	174	5.6	913	2	Q3KUR8_ONCMY	Q3kur8	oncorhynch
1130	177	5.6	1370	2	Q58NA4_APIME	Q58na4	aedes mellif	1203	174	5.6	951	1	LGR4_RAT	Q9z2h4	rattus norv
1131	176.5	5.6	185	2	Q2VGE5_PETMA	Q2vge5	petromyzon	1204	174	5.6	1361	2	Q17FX0_AEDAE	Q17fx0	aedes aegyp
1132	176.5	5.6	187	2	Q6E4M0_PETMA	Q6e4m0	petromyzon	1205	174	5.6	1367	2	Q1RMC9_HUMAN	Q1rmc9	homo sapien
1133	176.5	5.6	195	2	Q2VGT9_PETMA	Q2vgt9	petromyzon	1206	174	5.6	1371	2	Q1RMD0_HUMAN	Q1rmd0	homo sapien
1134	176.5	5.6	322	2	Q3R2R0_EPTBU	Q3r2r0	epitretus	1207	173.5	5.5	161	2	Q2VH22_PETMA	Q2vh22	petromyzon
1135	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46	oryza sativ	1208	173.5	5.5	261	2	Q5M8T1_HUMAN	Q5m8t1	homo sapien
1136	176.5	5.6	522	1	AMGO2_HUMAN	Q86sj2	homo sapien	1209	173.5	5.5	337	2	Q4RJX0_TETNG	Q4rjx0	tetraodon n
1137	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6	homo sapien	1210	173.5	5.5	353	2	Q640B1_XENTR	Q640b1	xenopus tro
1138	176.5	5.6	628	2	Q7PVZ6_ANOGA	Q7pvz6	anopheles g	1211	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8	xenopus lae
1139	176.5	5.6	856	2	Q59H17_PIG	Q59h17	sus scrofa	1212	173.5	5.5	421	1	OMD_HUMAN	Q9983	homo sapien
1140	176.5	5.6	901	2	Q4SBD4_TETNG	Q4sbd4	tetraodon n	1213	173.5	5.5	440	2	Q5TEF4_HUMAN	Q5tef4	homo sapien
1141	176.5	5.6	1495	1	LRCR7_RAT	P70587	rattus norv	1214	173.5	5.5	440	2	Q7TQ25_RAT	Q7tq25	rattus norv
1142	176	5.6	220	2	Q2VH09_PETMA	Q2vh09	petromyzon	1215	173.5	5.5	537	1	LG14_MOUSE	Q8k1s1	mus musculus
1143	176	5.6	249	2	Q4SUM4_TETNG	Q4sum4	tetraodon n	1216	173.5	5.5	537	2	Q3UVI9_MOUSE	Q3uvi9	mus musculus
1144	176	5.6	503	2	Q8LJ87_ORYSA	Q8lj87	oryza sativ	1217	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21	bos taurus
1145	176	5.6	623	2	Q9SE21_DROME	Q9se21	drosophila	1218	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5	mus musculus
1146	176	5.6	862	2	Q5GR02_CHICK	Q5gr02	gallus gall	1219	173.5	5.5	826	1	TLR4_PAPAN	Q7tsp2	papio anubi
1147	176	5.6	904	2	Q5TJ59_BOVIN	Q5tj59	bos taurus	1220	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720	fugu rubrip
1148	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58	bos taurus	1221	173.5	5.5	1167	2	Q16XG0_AEDAE	Q16xg0	aedes aegyp
1149	176	5.6	906	2	Q4SRZ0_TETNG	Q4srz0	tetraodon n	1222	173.5	5.5	1681	2	Q299Y2_DROPS	Q299y2	drosophila
1150	176	5.6	913	2	Q1PA38_ONCMY	Q1pa38	oncorhynch	1223	173	5.5	168	2	Q2VXK8_PETMA	Q2vxk8	petromyzon
1151	176	5.6	1032	1	TLR9_CANFA	Q5i2m8	canis fami	1224	173	5.5	192	2	Q2VHA2_PETMA	Q2vha2	petromyzon
1152	176	5.6	1257	2	Q9VK28_DROME	Q9vk28	drosophila	1225	173	5.5	192	2	Q2VGG5_PETMA	Q2vgs5	petromyzon
1153	176	5.6	1412	1	LAP2_HUMAN	Q96rt1	homo sapien	1226	173	5.5	194	2	Q2VHC8_PETMA	Q2vhc8	petromyzon
1154	175.5	5.6	167	2	Q2VXJ8_PETMA	Q2vxj8	petromyzon	1227	173	5.5	252	2	Q4G1I4_EPTST	Q4g1i4	epitretus
1155	175.5	5.6	185	2	Q2VWG3_PETMA	Q2vvg3	petromyzon	1228	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2	petromyzon
1156	175.5	5.6	251	2	Q2YE03_EPTST	Q2ye03	epitretus	1229	173	5.5	360	1	PGS2_HORSE	Q6e42	equus cabal
1157	175.5	5.6	272	2	Q4KPL4_9PETR	Q4kpl4	ichthyomyzo	1230	173	5.5	470	2	Q9V354_DROME	Q9v354	drosophila
1158	175.5	5.6	324	2	Q3R2R0_EPTBU	Q3r2r0	epitretus	1231	173	5.5	539	2	Q5O3F6_BRARE	Q5o3f6	brachydanio
1159	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4	tetraodon n	1232	173	5.5	664	2	Q5UT54_SALSA	Q5ut54	salmo salar
1160	175.5	5.6	440	2	Q7TMM3_RAT	Q7tmm3	rattus norv	1233	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40	mus musculus
1161	175.5	5.6	492	1	ANG01_MOUSE	Q80zd8	mus musculu	1234	173	5.5	892	2	Q466H0_METBF	Q466h0	methanosarc
1162	175.5	5.6	816	2	Q29L68_DROPS	Q29l68	drosophila	1235	173	5.5	925	1	GLHR_ANTIPL	P35409	anthopieura
1163	175.5	5.6	841	2	Q2V898_BOSTR	Q2v898	boselaphus	1236	173	5.5	1459	2	Q7Q0C5_ANOGA	Q7q0c5	anopheles g
1164	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718	fugu rubrip	1237	173	5.5	1459	2	Q8WRE4_ANOGA	Q8wre4	anopheles g
1165	175.5	5.6	1490	1	LRCR7_MOUSE	Q80te7	mus musculu	1238	172.5	5.5	161	2	Q2VHB2_PETMA	Q2vhb2	petromyzon
1166	175.5	5.6	1731	2	Q4S0D3_TETNG	Q4s0d3	tetraodon n	1239	172.5	5.5	161	2	Q2VGH1_PETMA	Q2vgh1	petromyzon
1167	175	5.6	168	2	Q2VHC0_PETMA	Q2vhc0	petromyzon	1240	172.5	5.5	163	2	Q6E4E2_PETMA	Q6e4e2	petromyzon
1168	175	5.6	192	2	Q2VH74_PETMA	Q2vh74	petromyzon	1241	172.5	5.5	171	2	Q2VHC2_PETMA	Q2vhc2	petromyzon
1169	175	5.6	192	2	Q2VKG6_PETMA	Q2vkg6	petromyzon	1242	172.5	5.5	237	2	Q2YE13_EPTST	Q2ye13	epitretus
1170	175	5.6	252	2	Q4GLJ2_EPTST	Q4glj2	epitretus	1243	172.5	5.5	259	2	Q2YE22_EPTST	Q2ye22	epitretus
1171	175	5.6	297	2	Q3Q2O0_EPTBU	Q3q2o0	epitretus	1244	172.5	5.5	353	1	KERA_CHICK	Q4235	gallus gall
1172	175	5.6	323	2	Q3R2R31_EPTBU	Q3r2r31	epitretus	1245	172.5	5.5	353	1	KERA_COTJA	Q9d66	coturnix co
1173	175	5.6	343	1	LUM_CHICK	P51890	gallus gall	1246	172.5	5.5	359	1	PGS2_HUMAN	P07585	homo sapien
1174	175	5.6	474	2	Q290X6_DROPS	Q290x6	drosophila	1247	172.5	5.5	359	1	PGS2_PANTR	Q5riv9	pan troglod
1175	175	5.6	510	2	Q9BGY6_MACFA	Q9bgy6	macaca fasc	1248	172.5	5.5	359	2	Q6FH10_HUMAN	Q6fh10	homo sapien
1176	175	5.6	512	2	Q17F18_AEDAE	Q17f18	aedes aegyp	1249	172.5	5.5	378	2	Q5R294_DROSI	Q5r294	drosophila
1177	175	5.6	905	2	Q3TM31_MOUSE	Q3tm31	mus musculu	1250	172.5	5.5	739	2	Q6ONV9_CABER	Q6onv9	caenorhabdi
1178	175	5.6	941	2	Q5H722_FUGRU	Q5h722	fugu rubrip	1251	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6	mus musculu
1179	175	5.6	973	2	Q6KCC7_ONCMY	Q6kcc7	oncorhynch	1252	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8	mus musculu
1180	175	5.6	1031	2	Q2EEY0_HORSE	Q2eey0	equus cabal	1253	172.5	5.5	1851	1	LAP4_DROME	Q7kry7	drosophila
1181	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1	anopheles g	1254	172.5	5.5	4256	2	Q8MJF3_CANFA	Q8mjf3	canis fami
1182	174.5	5.6	190	2	Q6E4E5_PETMA	Q6e4e5	petromyzon	1255	172	5.5	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
1183	174.5	5.6	191	2	Q2VGI5_PETMA	Q2vgi5	petromyzon	1256	172	5.5	347	1	TSK_BRARE	Q5848	brachydanio
1184	174.5	5.6	193	2	Q2VGD0_PETMA	Q2vgd0	petromyzon	1257	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
1185	174.5	5.6	440	2	Q4J5V4_AZOTI	Q4j5v4	azotobacter	1258	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5	homo sapien
1186	174.5	5.6	512	2	Q3CQ76_MOUSE	Q3cq76	m 8 days em	1259	172	5.5	904	2	Q1G1A3_BUBBU	Q1g1a3	bubalus bub
1187	174.5	5.6	567	2	Q4SL10_TETNG	Q4sl10	tetraodon n	1260	172	5.5	1134	2	Q65510_ARATH	Q65510	arabidopsis
1188	174.5	5.6	602	1	LRC40_MOUSE	Q9erc8	mus musculu	1261	172	5.5	1693	2	Q4INH4_GIBZE	Q4inh4	gibberella
1189	174.5	5.6	605	1	LRC40_XENLA	Q6gpj5	xenopus lae	1262	171.5	5.5	171	2	Q2VGJ0_PETMA	Q2vgj0	petromyzon
1190	174.5	5.6	795	1	TLR6_MOUSE	Q9epw9	mus musculu	1263	171.5	5.5	193	2	Q2VHD1_PETMA	Q2vhd1	petromyzon
1191	174.5	5.6	806	2	Q3UV88_MOUSE	Q3uv88	mus musculu	1264	171.5	5.5	195	2	Q2VH57_PETMA	Q2vh57	petromyzon
1192	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4	oryza sativ	1265	171.5	5.5	378	2	Q9V900_DROME	Q9v900	drosophila
1193	174.5	5.6	1060	2	Q6ZGM3_ORYSA	Q6zgm3	oryza sativ	1266	171.5	5.5	605	1	LRC40_XENTR	Q5m94	xenopus tro
1194	174	5.6	194	2	Q2VH35_PETMA	Q2vh35	petromyzon	1267	171.5	5.5	683	2	LRC4_HUMAN	Q75427	homo sapien
1195	174	5.6	196	2	Q2VGF0_PETMA	Q2vgf0	petromyzon	1268	171.5	5.5	791	2	Q2L8H0_LISMO	Q2l8h0	listeria mo
1196	174	5.6	299	2	Q3R2R28_EPTBU	Q3r2r28	epitretus	1269	171.5	5.5	858	1	LRC8D_RAT	Q5u308	rattus norv
1197	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5	tetraodon n	1270	171.5	5.5	858	1	TLR5_HUMAN	Q60502	homo sapien
1198	174	5.6	535	2	Q9RX50_BRANI	Q9rx50	brassica ni	1271	171.5	5.5	858	2	Q32MI3_HUMAN	Q32mi3	homo sapien
1199	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5	anopheles g	1272	171.5	5.5	858	2	Q32MI2_HUMAN	Q32mi2	homo sapien

1273	171.5	5.5	859	1	LRC8D_MOUSE	Q8bgr2	mus musculus	1346	168.5	5.4	343	2	Q501S3_BRARE	Q501s3	brachydanio
1274	171.5	5.5	859	2	Q3U170_MOUSE	Q3ti70	mus musculus	1347	168.5	5.4	353	2	Q7S1S8_XENIA	Q7s1s8	xenopus lae
1275	171.5	5.5	1589	2	Q9U0Q9_METAN	Q9u0q9	metarhizium	1348	168.5	5.4	363	2	Q8C8A7_MOUSE	Q8c8a7	mus musculus
1276	171	5.5	168	2	Q2VHF6_PETMA	Q2vhf6	petromyzon	1349	168.5	5.4	366	2	Q3UGP9_MOUSE	Q3ugp9	mus musculus
1277	171	5.5	192	2	Q2VGS2_PETMA	Q2vgs2	petromyzon	1350	168.5	5.4	378	2	Q5R264_DROSE	Q5r264	drosofila
1278	171	5.5	194	2	Q2VGS3_PETMA	Q2vgs3	petromyzon	1351	168.5	5.4	619	2	Q6K8K0_ORYSA	Q6k8k0	oryza sativ
1279	171	5.5	299	2	Q3Z0Z7_EPTBU	Q3z0z7	epitretus	1352	168.5	5.4	685	2	Q6F545_LISMO	Q6f545	listeria mo
1280	171	5.5	354	2	Q3TSV1_MOUSE	Q3tsv1	mus musculus	1353	168.5	5.4	694	2	Q6I1P91_CAEBR	Q6i1p91	caenorhabdi
1281	171	5.5	360	1	PGS2_PTG	Q9xsd9	sus scrofa	1354	168.5	5.4	728	2	Q8KTF6_LISMO	Q8ktf6	listeria mo
1282	171	5.5	360	1	Q6DV11_GECJA	Q6dv11	gecko japon	1355	168.5	5.4	744	2	Q8LH86_LISMO	Q8lh86	listeria mo
1283	171	5.5	469	2	Q3URB9_MOUSE	Q3urb9	mus musculus	1356	168.5	5.4	791	2	Q4EQX8_LISMO	Q4eqx8	listeria mo
1284	171	5.5	512	2	Q17F19_AEDAE	Q17f19	aedes aegypt	1357	168.5	5.4	800	2	Q4EQX8_LISMO	Q4eqx8	listeria mo
1285	171	5.5	517	2	Q17K69_AEDAE	Q17k69	aedes aegypt	1358	168.5	5.4	1036	2	Q9FN37_ARATH	Q9fn37	arabidopsis
1286	171	5.5	643	2	Q502J4_BRARE	Q502j4	brachydanio	1359	168.5	5.4	1360	2	Q9NDI1_DROME	Q9ndi1	drosofila
1287	171	5.5	833	1	TLR4_FELCA	P58727	felis silve	1360	168.5	5.4	1724	2	Q4H4B6_BRARE	Q4h4b6	brachydanio
1288	171	5.5	976	2	Q3VIN1_MOUSE	Q3vin1	mus musculus	1361	168.5	5.4	3201	2	Q2QBE0_9ALPH	Q2qbe0	cercopitheco
1289	171	5.5	976	2	Q3TAN2_MOUSE	Q3tan2	mus musculus	1362	168.5	5.4	351	2	Q32N68_XENIA	Q32n68	xenopus lae
1290	171	5.5	1091	2	Q17L59_AEDAE	Q17l59	aedes aegypt	1363	168.5	5.4	351	2	Q65YW8_XENIA	Q65yw8	xenopus lae
1291	171	5.5	1317	2	Q5TUS9_ANOGA	Q5tus9	anopheles g	1364	168.5	5.4	369	2	Q28X02_DROPS	Q28x02	drosofila
1292	170.5	5.4	185	2	Q2VGH0_PETMA	Q2vgh0	petromyzon	1365	168.5	5.4	402	2	Q72U35_LEPIC	Q72u35	leptospira
1293	170.5	5.4	246	2	Q6B4J1_PETMA	Q6b4j1	petromyzon	1366	168.5	5.4	539	2	Q16K00_AEDAE	Q16k00	aedes aegypt
1294	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2	macaca fasc	1367	168.5	5.4	773	2	Q5NE35_LISMO	Q5ne35	listeria mo
1295	170.5	5.4	373	1	ASPEN_MOUSE	Q9nmg4	mus musculus	1368	168.5	5.4	951	1	LGR4_HUMAN	Q9bxb1	homo sapien
1296	170.5	5.4	741	2	Q8KTF7_LISMO	Q8ktf7	listeria mo	1369	168.5	5.4	977	2	Q8GVW0_ORYSA	Q8gvw0	oryza sativ
1297	170.5	5.4	761	2	Q3XNG0_9PROT	Q3xng0	magnetococ	1370	168.5	5.4	1050	2	Q2L4T3_CANFA	Q2l4t3	canis famila
1298	170.5	5.4	794	2	Q2L8H9_LISMO	Q2l8h9	listeria mo	1371	168.5	5.4	147	2	Q9TT00_PIG	Q9tt00	sus scrofa
1299	170.5	5.4	1031	1	TLR9_FELCA	Q5i2m7	felis silve	1372	167.5	5.3	171	2	Q2VHCL_PETMA	Q2vhcl	petromyzon
1300	170.5	5.4	2145	1	CYAA_PODAN	Q01513	podospora a	1373	167.5	5.3	185	2	Q2VGV4_PETMA	Q2vgv4	petromyzon
1301	170	5.4	187	2	Q6E4D9_PETMA	Q6e4d9	petromyzon	1374	167.5	5.3	351	1	KERA_MOUSE	Q35367	mus musculus
1302	170	5.4	192	2	Q2VGM4_PETMA	Q2vgm4	petromyzon	1375	167.5	5.3	360	1	PGS2_SHEEP	Q9tt62	ovis aries
1303	170	5.4	192	2	Q2VGH0_PETMA	Q2vgh0	petromyzon	1376	167.5	5.3	378	2	Q72U36_LEPIC	Q72u36	leptospira
1304	170	5.4	192	2	Q2VGG2_PETMA	Q2vgs2	petromyzon	1377	167.5	5.3	396	2	Q8C3D9_MOUSE	Q8c3d9	mus musculus
1305	170	5.4	192	2	Q2VGI9_PETMA	Q2vgi9	petromyzon	1378	167.5	5.3	422	1	QMD_BOVIN	Q77742	bos taurus
1306	170	5.4	364	1	LRLC19_MOUSE	Q8bzt5	mus musculus	1379	167.5	5.3	550	2	Q2QXR6_ORYSA	Q2qx6	oryza sativ
1307	170	5.4	415	2	Q295B8_DROPS	Q295b8	drosofila	1380	167.5	5.3	568	2	Q16M66_AEDAE	Q16m66	aedes aegypt
1308	170	5.4	473	2	Q3TSSQ3_MOUSE	Q3tsg3	mus musculus	1381	167.5	5.3	694	2	Q4RYL2_TETNG	Q4ryl2	tetradon n
1309	170	5.4	545	2	Q1EGK2_FUGRU	Q1egk2	fugu rubrip	1382	167.5	5.3	907	2	Q3V1L2_MOUSE	Q3v1l2	mus musculus
1310	170	5.4	572	2	Q4QGJ6_LEIMA	Q4qgj6	leishmania	1383	167.5	5.3	917	2	Q75GM9_ORYSA	Q75gm9	oryza sativ
1311	170	5.4	883	2	Q4VAM0_HUMAN	Q4van0	homo sapien	1384	167.5	5.3	1174	2	Q25AQ0_ORYSA	Q25aq0	oryza sativ
1312	170	5.4	907	1	LGR5_HUMAN	Q75473	homo sapien	1385	167.5	5.3	1225	2	Q16V17_AEDAE	Q16v17	aedes aegypt
1313	170	5.4	907	2	Q4VAM2_HUMAN	Q4vam2	homo sapien	1386	167.5	5.3	168	2	Q2VGM8_PETMA	Q2vgm8	petromyzon
1314	170	5.4	1024	2	Q84IE6_RALSO	Q84ie6	ralstonia s	1387	167.5	5.3	262	2	Q2YE18_EPTST	Q2ye18	epitretus
1315	170	5.4	1032	2	Q59ER8_HUMAN	Q59er8	homo sapien	1388	167.5	5.3	537	2	Q6P2A4_RAT	Q6p2a4	rattus norv
1316	169.5	5.4	167	2	Q2VGL5_PETMA	Q2vgl5	petromyzon	1389	167.5	5.3	582	2	Q6AY15_RAT	Q6ay15	rattus norv
1317	169.5	5.4	173	2	Q2VGD2_PETMA	Q2vgd2	petromyzon	1390	167.5	5.3	633	2	Q8F3F6_LEPIN	Q8f3f6	leptospira
1318	169.5	5.4	352	1	KERA_BOVIN	Q62702	bos taurus	1391	167.5	5.3	743	2	Q84CF7_LISMO	Q84cf7	listeria mo
1319	169.5	5.4	366	2	Q8BX06_MOUSE	Q8bx06	mus musculus	1392	167.5	5.3	777	2	Q282P9_DROPS	Q282p9	drosofila
1320	169.5	5.4	463	2	Q2LYW7_DROPS	Q2lyw7	drosofila	1393	167.5	5.3	838	1	TLR4_CRIGR	Q9wv82	cricetus
1321	169.5	5.4	493	1	AMG01_RAT	Q80z47	rattus norv	1394	167.5	5.3	886	2	Q469S7_METBF	Q469s7	methanosarc
1322	169.5	5.4	651	2	Q4T8T9_TETNG	Q4t8t9	tetradon n	1395	167.5	5.3	939	2	Q4SZU0_TETNG	Q4szu0	tetradon n
1323	169.5	5.4	760	2	Q9TOK5_ARATH	Q9tok5	arabidopsis	1396	167.5	5.3	1112	2	Q4G2W2_LYCPM	Q4g2w2	lycopersico
1324	169.5	5.4	876	2	Q67WE5_ORYSA	Q67we5	oryza sativ	1397	167.5	5.3	1112	2	Q41397_LYCPM	Q41397	lycopersico
1325	169.5	5.4	991	1	FLII_MOUSE	Q9fj28	mus musculus	1400	167.5	5.3	1112	2	Q41398_LYCPM	Q41398	lycopersico
1326	169.5	5.4	1271	1	FLII_MOUSE	Q9fj28	mus musculus	1401	167.5	5.3	1263	2	Q4SID1_TETNG	Q4sid1	tetradon n
1327	169.5	5.4	1545	2	Q29P78_DROPS	Q29p78	drosofila	1402	167.5	5.3	1845	2	Q5QNO9_MOUSE	Q5qnq9	mus musculus
1328	169	5.4	168	2	Q2VGO9_PETMA	Q2vg9	petromyzon	1403	167.5	5.3	163	2	Q6E4D4_PETMA	Q6e4d4	petromyzon
1329	169	5.4	217	2	Q66WJ6_FELCA	Q66wj6	felis silve	1404	167.5	5.3	185	2	Q2VGV9_PETMA	Q2vgv9	petromyzon
1330	169	5.4	273	2	Q5XPY6_ICTPU	Q5xpy6	ictalurus p	1405	166.5	5.3	351	2	Q3KQ16_XENIA	Q3kq16	xenopus lae
1331	169	5.4	279	2	Q58HK2_TRASC	Q58hk2	trachemys s	1406	166.5	5.3	370	2	Q3ZBN5_BOVIN	Q3zbn5	bos taurus
1332	169	5.4	354	1	PGS2_MOUSE	Q28654	mus musculus	1407	166.5	5.3	483	2	Q5NE36_LISMO	Q5ne36	listeria mo
1333	169	5.4	354	2	Q3UKR1_MOUSE	Q3ukr1	m 14 days p	1408	166.5	5.3	549	2	Q9SVW8_ARATH	Q9svw8	arabidopsis
1334	169	5.4	360	2	Q6J0Y6_PAROL	Q6j0y6	paralichthy	1409	166.5	5.3	582	2	Q5R423_PONPY	Q5r423	pongo pygma
1335	169	5.4	757	2	Q9RMS7_ORYSA	Q9rms7	oryza sativ	1410	166.5	5.3	601	2	Q16P98_AEDAE	Q16p98	aedes aegypt
1336	169	5.4	839	2	Q9RXS7_DEIRA	Q9rxs7	deinococcus	1411	166.5	5.3	739	2	Q84CF6_LISMO	Q84cf6	listeria mo
1337	169	5.4	1175	2	Q4RER3_TETNG	Q4rer3	tetradon n	1412	166.5	5.3	741	2	Q8KTF0_LISMO	Q8ktf0	listeria mo
1338	169	5.4	1288	2	Q624K5_CAEBR	Q624k5	caenorhabdi	1413	166.5	5.3	743	2	Q95RV9_DROME	Q95rv9	drosofila
1339	169	5.4	1658	2	Q4PLE9_GIBTN	Q4ple9	gibberella	1414	166.5	5.3	743	2	Q8KTF1_LISMO	Q8ktf1	listeria mo
1340	168.5	5.4	169	2	Q2VH97_PETMA	Q2vh97	petromyzon	1415	166.5	5.3	744	2	Q8KTF1_LISMO	Q8ktf1	listeria mo
1341	168.5	5.4	184	2	Q2VGT2_PETMA	Q2vgt2	petromyzon	1416	166.5	5.3					
1342	168.5	5.4	185	2	Q2VGO5_PETMA	Q2vg05	petromyzon	1417	166.5	5.3					
1343	168.5	5.4	246	2	Q4KP10_LAMAP	Q4kp10	lampetra ap	1418	166.5	5.3					
1344	168.5	5.4	255	2	Q66WJ3_FELCA	Q66wj3	felis silve								
1345	168.5	5.4	333	2	Q4SVZ8_TETNG	Q4svz8	tetradon n								



1419	166.5	5.3	744	2	Q8KTF5_LISMO	Q8ktf5	listeria mo
1420	166.5	5.3	744	2	Q8KTF8_LISMO	Q8ktf8	listeria mo
1421	166.5	5.3	744	2	Q8KHNI_LISMO	Q8khn1	listeria mo
1422	166.5	5.3	744	2	Q8KTF8_LISMO	Q8ktf8	listeria mo
1423	166.5	5.3	746	2	Q8KTF3_LISMO	Q8ktf3	listeria mo
1424	166.5	5.3	792	2	Q5NE37_LISMO	Q5ne37	listeria mo
1425	166.5	5.3	794	2	Q2L8H1_LISMO	Q2l8h1	listeria mo
1426	166.5	5.3	794	2	Q2L8G9_LISMO	Q2l8g9	listeria mo
1427	166.5	5.3	794	2	Q2L8H5_LISMO	Q2l8h5	listeria mo
1428	166.5	5.3	794	2	Q2L8H2_LISMO	Q2l8h2	listeria mo
1429	166.5	5.3	794	2	Q2L8H7_LISMO	Q2l8h7	listeria mo
1430	166.5	5.3	794	2	Q2L8H4_LISMO	Q2l8h4	listeria mo
1431	166.5	5.3	794	2	Q2L8H3_LISMO	Q2l8h3	listeria mo
1432	166.5	5.3	797	2	Q4EJ83_LISMO	Q4ej83	listeria mo
1433	166.5	5.3	800	1	INLA_LISMF	Q723k6	listeria mo
1434	166.5	5.3	800	1	INLA_LISMO	P25146	listeria mo
1435	166.5	5.3	800	2	Q4SGD5_LISMO	Q4sgd5	listeria mo
1436	166.5	5.3	800	2	Q4SGD6_LISMO	Q4sgd6	listeria mo
1437	166.5	5.3	1012	2	Q95YI6_ASTPE	Q95yi6	asterina pe
1438	166.5	5.3	1115	2	Q652D9_ORYSA	Q652d9	oryza sativ
1439	166.5	5.3	1215	2	Q60PY2_CABER	Q60py2	caenorhabdi
1440	166.5	5.3	1270	2	Q70HP7_ANOGA	Q70hp7	anopheles g
1441	166.5	5.3	1280	2	Q95YI7_ASTPE	Q95yi7	asterina pe
1442	166.5	5.3	3204	2	Q6X248_9ALPH	Q6x248	bovine herp
1443	166	5.3	163	2	Q6B4F8_PETMA	Q6b4f8	petromyzon
1444	166	5.3	170	2	Q2VGK9_PETMA	Q2vgk9	petromyzon
1445	166	5.3	192	2	Q2VGK1_PETMA	Q2vgk1	petromyzon
1446	166	5.3	245	2	Q4KP01_LAMAP	Q4kp01	lampetra ap
1447	166	5.3	393	2	Q3UTG8_MOUSE	Q3utg8	mus musculu
1448	166	5.3	426	2	Q72TC3_LEPIC	Q72tc3	leptospira
1449	166	5.3	768	2	Q4SSE3_TETNG	Q4sse3	tetraodon n
1450	166	5.3	806	2	Q6P690_RAT	Q6p690	rattus norv
1451	166	5.3	835	1	TLR4_RAT	Q9qx05	rattus norv
1452	166	5.3	971	2	TLR432_SALSA	Q2ah32	salmu salar
1453	166	5.3	1030	1	TLR29_PIG	Q5i2m3	sus scrofa
1454	166	5.3	1030	2	Q865R8_PIG	Q865r8	sus scrofa
1455	166	5.3	1110	2	Q7G768_ORYSA	Q7g768	oryza sativ
1456	166	5.3	1221	2	Q9N5Z3_CABEL	Q9n5z3	brachydanio
1457	166	5.3	2139	2	Q4PDW0_USTMA	Q4pdw0	ustilago ma
1458	165.5	5.3	161	2	Q2VGK0_PETMA	Q2vgk0	petromyzon
1459	165.5	5.3	169	2	Q2VHG0_PETMA	Q2vhg0	petromyzon
1460	165.5	5.3	195	2	Q2VGU2_PETMA	Q2vgu2	petromyzon
1461	165.5	5.3	327	2	Q5RHE5_BRARE	Q5rhe5	brachydanio
1462	165.5	5.3	360	1	PGS2_BOVIN	P21r793	bos taurus
1463	165.5	5.3	360	1	PGS2_CANEFA	Q29393	canis famil
1464	165.5	5.3	360	2	Q3WHN1_BOVIN	Q3whn1	bos taurus
1465	165.5	5.3	385	2	Q17EE7_ADEAE	Q17ee7	aedes aegypt
1466	165.5	5.3	526	2	Q7XJS3_ARATH	Q7xjs3	arabidopsis
1467	165.5	5.3	641	2	Q5H716_FUGRU	Q5h716	fugu rubrip
1468	165.5	5.3	1005	2	Q3L273_SPAAU	Q3l273	sparus aura
1469	165.5	5.3	1063	2	Q3L274_SPAAU	Q3l274	sparus aura
1470	165.5	5.3	1101	2	Q59H95_HUMAN	Q59h95	homo sapien
1471	165.5	5.3	1256	1	FLII_HUMAN	Q24020	drosophila
1472	165.5	5.3	1269	1	FLII_HUMAN	Q13405	homo sapien
1473	165.5	5.3	1269	2	Q5R4G9_PONPY	Q5r4g9	pongo pygma
1474	165	5.3	196	2	Q2VH02_PETMA	Q2vh02	petromyzon
1475	165	5.3	283	2	Q4RX02_TETNG	Q4rx02	tetraodon n
1476	165	5.3	436	2	Q5R6F8_PONPY	Q5r6f8	pongo pygma
1477	165	5.3	780	2	Q299R7_DROPS	Q299r7	drosophila
1478	165	5.3	902	2	Q7RYP2_NEUCR	Q7ryp2	neurospora
1479	165	5.3	955	2	Q3RNJ0_XENLA	Q3rnj0	xenopus lae
1480	165	5.3	994	2	Q9C637_ARATH	Q9c637	arabidopsis
1481	165	5.3	1135	2	Q7XS12_ORYSA	Q7xs12	oryza sativ
1482	165	5.3	1154	2	Q7QHH4_ANOGA	Q7qhh4	anopheles g
1483	164.5	5.2	171	2	Q2VH95_PETMA	Q2vh95	petromyzon
1484	164.5	5.2	185	2	Q2VGU7_PETMA	Q2vgu7	petromyzon
1485	164.5	5.2	235	2	Q4GLH9_EPTST	Q4glh9	eptatretus
1486	164.5	5.2	437	2	Q1BQ30_9BURK	Q1bq30	burkholderi
1487	164.5	5.2	468	2	Q4LVE2_9BURK	Q4lve2	burkholderi
1488	164.5	5.2	582	1	SHOC2_HUMAN	Q9uq13	homo sapien
1489	164.5	5.2	582	2	Q5VZS9_HUMAN	Q5vzs9	homo sapien
1490	164.5	5.2	582	2	Q5RAV5_PONPY	Q5rav5	pongo pygma
1491	164.5	5.2	734	2	Q5R7N1_PONPY	Q5r7n1	pongo pygma

## RESULT 1

ID	VASN_HUMAN	STANDARD;	PRT;	673 AA.
AC	Q6EMK4; Q6UXL4; Q6UXL5; Q96CX1;			
DT	18-APR-2006, integrated into UniProtKB/Swiss-Prot.			
DT	16-AUG-2004, entry version 1.			
DT	25-JUL-2006, entry version 17.			
DE	Vasorin precursor (Protein Slit-like 2).			
GN	Names:VASN; Synonyms:SLITL2; ORFNames:UNQ314/PRO357/PRO1282;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;			
OC	Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, INTERACTION WITH TGFBI; TGFBI2			
RP	AND TGFBI3, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND			
RP	GLYCOSYLATION.			
RX	PubMed=15247411; DOI=10.1073/pnas.0404117101;			
RA	Ikeda Y., Inai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaoka T.,			
RA	Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,			
RA	Nagai R., Kitamura T.;			
RT	"Vasorin, a transforming growth factor beta-binding protein expressed			
RT	in vascular smooth muscle cells, modulates the arterial response to			
RT	injury in vivo.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-384.			
RX	MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R.L., Watanabe C., Wileand D., Woods K., Xie M.-H.,			
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-384.			
RC	TISSUE=Lung, and Placenta;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heist F.,			
RA	Diatchenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

## ALIGNMENTS

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marta M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RN GLYCOSYLATION [LARGE SCALE ANALYSIS] AT ASN-117 AND ASN-273, AND MASS  
 RP SPECTROMETRY.  
 RX PubMed:16335952; DOI=10.1021/pr0502065;  
 RA Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,  
 RA Moore R.J., Smith R.D.;  
 RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,  
 RT hydrazide chemistry, and mass spectrometry.";  
 RL J. Proteome Res. 4:2070-2080 (2005).  
 CC -!- FUNCTION: May act as an inhibitor of TGF-beta signaling.  
 CC -!- SUBUNIT: Interacts with TGFBI, TGFBI2 and TGFBI3.  
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein (Probable). Secreted protein.  
 CC -!- TISSUE SPECIFICITY: Expressed at highest levels in aorta, at  
 CC intermediate levels in kidney and placenta and at lowest levels in  
 CC brain, heart, liver, lung and skeletal muscle. Within the aorta,  
 CC the strongest expression is found in the tunica media of the  
 CC proximal ascending aorta, the descending thoracic aorta, the  
 CC abdominal aorta and the coronary arteries. Within the kidney,  
 CC expression is found in the interstitial cells.  
 CC -!- PTM: N-glycosylated.  
 CC -!- SIMILARITY: Contains 1 EGF-like domain.  
 CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.  
 CC -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.  
 CC  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 -----  
 DR EMBL; AY166584; RAO27704.1; -; mRNA.  
 DR EMBL; AY358298; RAO88665.1; -; mRNA.  
 DR EMBL; AY358299; RAO88666.1; -; mRNA.  
 DR EMBL; BC013767; RAO13767.1; -; mRNA.  
 DR EMBL; BC068575; RAO68575.1; -; mRNA.  
 DR UniGene; Hs.372579; -;  
 DR HSSP; Q9BZR6; 1P8T.  
 DR Ensembl; ENSG00000168140; Homo sapiens.  
 DR HGNC; HGNC:18517; VASN.  
 DR MIM; 608843; Gene.  
 DR RZPD-ProteExp; IOH40553; -;  
 DR InterPro; IPR006210; EGF.  
 DR InterPro; IPR000742; EGF\_3.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR013032; EGF\_like\_reg.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_C.  
 DR InterPro; IPR000372; LRR\_cys\_N.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00008; EGF\_1.  
 DR Pfam; PF00841; fn3; 1.  
 DR Pfam; PF00560; LRR\_1; 8.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00369; LRR\_TYP; 2.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS00853; FN3; 1.  
 DR EGF-like domain; glycoprotein; Leucine-rich repeat; Membrane;  
 KW Polymorphism; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 23 potential.

FT	CHAIN	24	673	Vasorin. /FTID=PRO_0000232630. Extracellular (Potential). Potential. Cytoplasmic (Potential). LRR 1. LRR 2. LRR 3. LRR 4. LRR 5. LRR 6. LRR 7. LRR 8. LRR 9. LRR 10. LRR 11. EGF-like. Fibronectin type-III. N-linked (GlcNAc... ) (Potential). N-linked (GlcNAc... ) N-linked (GlcNAc... ) N-linked (GlcNAc... ) (Potential). N-linked (GlcNAc... ) (Potential). By similarity. By similarity. E -> A (in dBSNP:3810818). /FTID=VAR_025991. G -> S (in Ref. 2; AAQ88665). Missing (in Ref. 2; AAQ88665). 891E149652DEA286 CRC64;
FT	TOPO_DOM	24	575	
FT	TRANSMEM	576	596	
FT	TOPO_DOM	597	673	
FT	REPEAT	51	74	
FT	REPEAT	75	98	
FT	REPEAT	100	122	
FT	REPEAT	123	146	
FT	REPEAT	148	168	
FT	REPEAT	169	191	
FT	REPEAT	193	214	
FT	REPEAT	215	240	
FT	REPEAT	241	263	
FT	REPEAT	264	289	
FT	REPEAT	290	310	
FT	DOMAIN	405	442	
FT	DOMAIN	458	555	
FT	CARBOHYD	101	101	
FT	CARBOHYD	117	117	
FT	CARBOHYD	273	273	
FT	CARBOHYD	500	500	
FT	CARBOHYD	528	528	
FT	DISULFID	409	420	
FT	DISULFID	414	430	
FT	DISULFID	432	441	
FT	VARIANT	384	384	
FT	CONFLICT	70	70	
FT	CONFLICT	91	165	
FT	SEQUENCE	673 AA;	71713 MW;	891E149652DEA286 CRC64;
Qy	Query Match	98.2%;	Score 3078.5;	DB 1; Length 673;
Db	Best Local Similarity	88.6%;	Pred. No. 1.8e-166;	
Qy	Matches	596;	Conservative	0; Mismatches 2; Indels 75; Gaps 1;
Qy	1	MCSRVPPLLELLALLALPGVQCPCGSCQCSQPTVFCTARQGTTPRDPVPPDTVGLYVF	60	
Db	1	MCSRVPPLLELLALLALPGVQCPCGSCQCSQPTVFCTARQGTTPRDPVPPDTVGLYVF	60	
Qy	61	ENGITMLDASSFAGLPGLQLLDLSQNIAS-----	90	
Db	61	ENGITMLDAGSFAGLPGLQLLDLSQNIASLPSCVGFQFQLANLSNLDLTANRLHEITNETF	120	
Qy	91	-----LRLPRLLLDLSHNS	105	
Db	121	RGLRRLRYLGNRRIRHIQPGAPDTRDLLELKLQNEURLALPRLPRLLLDLSHNS	180	
Qy	106	LLALEPGILDTANVEALRLAGLGLQQLDEGLFSLRLNLDLDVSDNQLERVPVIRGLRG	165	
Db	181	LLALEPGILDTANVEALRLAGLGLQQLDEGLFSLRLNLDLDVSDNQLERVPVIRGLRG	240	
Qy	166	LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGSLPRLLLAAARNPF	225	
Db	241	LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGSLPRLLLAAARNPF	300	
Qy	226	NCVCPLSWFGPWVRESHVTLASPEETRCHEPPKNAGRLILLELDYADFCGPTATTTATVPT	285	
Db	301	NCVCPLSWFGPWVRESHVTLASPEETRCHEPPKNAGRLILLELDYADFCGPTATTTATVPT	360	
Qy	286	TRPVVREPTALSSSLAFTWLSPTAPATEAPSPSTAPPTVGVFPQDPCPSTCLNGGTC	345	
Db	361	TRPVVREPTALSSSLAFTWLSPTAPATEAPSPSTAPPTVGVFPQDPCPSTCLNGGTC	420	
Qy	346	HLGTRHHLACLPBGFTGLYCESQMGQGTSPPTVTPRPPRSLTLGIEPVSPSLRVGL	405	
Db	421	HLGTRHHLACLPBGFTGLYCESQMGQGTSPPTVTPRPPRSLTLGIEPVSPSLRVGL	480	
Qy	406	QRYLQSSVQLRLRLTYRNLSGDKELVTLRLPASLAETVTLRPNATYSCVMPGLGP	465	
Db	481	QRYLQSSVQLRLRLTYRNLSGDKELVTLRLPASLAETVTLRPNATYSCVMPGLGP	540	
Qy	466	GRVPEGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAAVGAAYCVR	525	



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Db 541 GRVPGEACGGAHTPPAVHSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
Qy 526 RGRMAAAQAQDQGVGPGAGPLEGKVPLEPGPKATGGGEGALPSGSECEVPLMGFFPG 585
Db 601 RGRMAAAQAQDQGVGPGAGPLEGKVPLEPGPKATGGGEGALPSGSECEVPLMGFFPG 660
Qy 586 PGLQSPFLHAKPYI 598
Db 661 PGLQSPFLHAKPYI 673

RESULT 2
VASN MOUSE
ID VASN MOUSE STANDARD; PRT; 673 AA.
AC Q9CZT5; Q8BJJO; Q8R2G5;
DT 18-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 18-APR-2006, sequence version 2.
DT 13-JUN-2006, entry version 29.
DE vasorin precursor (Protein Slit-like 2).
GN Name=Vasn; Synonyms=Slit12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C57BL/6J;
RA Schrewe H., Kutejova E.;
RT "Structure and expression analysis of the mouse Slit-like 2 (slitl2) gene.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler S., Aturaliya R.N., Bailey T.L.,
RA Bansal K., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humnietcki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Moutagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamashiki H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Bruscia V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,

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RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP DEVELOPMENTAL STAGE, AND INDUCTION.
RX PubMed=15247411; DOI=10.1073/pnas.0404117101;
RA Ikeda Y., Inai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaoka T.,
RA Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,
RA Nagai R., Kitamura T.;
RT "Vasorin, a transforming growth factor beta-binding protein expressed
RT in vascular smooth muscle cells, modulates the arterial response to
RT injury in vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).
CC -!- FUNCTION: May act as an inhibitor of TGF-beta signaling (By
CC similarity).
CC -!- SUBUNIT: Interacts with TGFBI, TGFBI2 and TGFBI3 (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (Probable).
CC -!- DEVELOPMENTAL STAGE: Expression begins at E10.5 and increases as
CC development progresses to E17.5. Expression rises in parallel with
CC the differentiation of vascular smooth muscle cells (VSMCs) of the
CC aorta.
CC -!- INDUCTION: Upon retinoic acid-induced differentiation of smooth
CC muscle cells in vitro.
CC -!- PTM: N-glycosylated (By similarity).
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AJ458938; CAD30331.1; -; mRNA.
DR EMBL: AK012169; BAB28075.1; -; mRNA.
DR EMBL: AK083684; BAC38992.1; -; mRNA.
DR EMBL: AK132325; BAE21105.1; -; mRNA.
DR EMBL: BC050274; AAH50274.1; -; mRNA.
DR UniGene: Mm.248337; -.
DR HSSP: P00740; LEDM.
DR Ensembl: ENSMUSG00000039646; Mus musculus.
DR MGI: MGI:2177651; Vasn.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.

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DR InterPro; IPR000372; LRR_cys_N.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00369; LRR_TYP; 7.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50853; FN3; 1.
KW EGF-like domain; Glycoprotein; Leucine-rich repeat; Membrane; Repeat;
KW SIGNAL; 1 24
FT CHAIN 25 673
FT /FTID=PRO_0000232631.
FT TOPO_DOM 25 576 Extracellular (Potential).
FT TRANSMEM 577 597 Potential.
FT TOPO_DOM 598 673 Cytoplasmic (potential).
FT REPEAT 52 75 LRR 1.
FT REPEAT 76 99 LRR 2.
FT REPEAT 101 123 LRR 3.
FT REPEAT 124 147 LRR 4.
FT REPEAT 149 169 LRR 5.
FT REPEAT 170 192 LRR 6.
FT REPEAT 194 215 LRR 7.
FT REPEAT 216 241 LRR 8.
FT REPEAT 242 264 LRR 9.
FT REPEAT 265 287 LRR 10.
FT REPEAT 289 311 LRR 11.
FT DOMAIN 406 443 EGF-like.
FT DOMAIN 459 556 Fibronectin type-III.
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 118 118 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 274 274 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 501 501 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 555 555 N-linked (GlcNAc...) (Potential).
FT DISULFID 410 421 By similarity.
FT DISULFID 415 431 By similarity.
FT DISULFID 433 442 By similarity.
FT CONFLICT 225 225 S -> Y (in Ref. 2; BAB28075).
FT CONFLICT 383 383 L -> H (in Ref. 2; BAC38992).
SQ SEQUENCE 673 AA; 72261 MW; AAB8DA82DA8E9D32 CRC64;

Query Match 79.4%; Score 2490; DB 1; Length 673;
Best Local Similarity 73.5%; Pred. No. 4.6e-133;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;

QY 6 PLLLLPLLHLLGPGVQCSPGCGCCQCPQTVFCTARQGTTPRDPDVTGLYVFENGIT 65
Db 9 PLL--L--LLLVLLGSGVQCSPGCGCCQCPQTVFCTARQGTTPRDPDVTGLYVFENGIT 66

QY 66 MLDASSFAGLPGLQLLDLSQNIAS----- 90
Db 67 TLDVCGFAGLPGLQLLDLSQNIATSPGGIFQPLVNLNLDLTANKLHEISNETFRGLRR 126
QY 91 -----LRLPRLLDLSNLSLALE 110
Db 127 LERLYLGNKRIRHIOPCAFDALDRLLLEKLPLDPNELRVLPPLHPLRLLLDLSHNSIPALE 186
QY 111 PGLDTPANVEARLGLGLQQLDEGLFSRLNLDLDVSDNQLERVPVIRGLGLTLRL 170
Db 187 AGLDTPANVEARLGLGLQQLDEGLFGRLLNLDLDVSDNQLHMPSVIQGLRGLTLRL 246
QY 171 LAGNTRIAQIRPDLAQLALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCP 230

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Db 247 LAGNTRIAQIRPDLAQLALQELDVSNLSLQALPSDLSLFPRLRLAAARNPFNCVCP 306
QY 231 LSWFGFWVRESHVTLASPEETRCHFFPPKNAGRLLLELDYADFQCPATTTTATVPTTRPVV 290
Db 307 LSWFGFWVRENHVVLASPEETRCHFFPPKNAGRLLLDLDYADFQCPVTTTATVPTIRSTI 366
QY 291 REPTALSSSLAPTWSLPTAPATEAPSPSTAPTPTGVPQPOPCDPSTCLNGTCHLGTTR 350
Db 367 REPTLSTSSQAPTWPSTLPTTQASTVLSTAPPTMRPAQPOPCDPASICLNGGSCRIGAR 426
QY 351 HHLACLCPGEGFTGLYCESQMGQGTSPPTVTPRPSRLTLGTIEPVSPTSLRVLQRYLQ 410
Db 427 HHWECLCPGEGFGLYCSPVQGMKPSIPDTPRPPPLPLSLTEPVSPTSLRVLQRYLQ 486
QY 411 GSSVQLRSLRLTYRNLSGDPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPGLQGRVPE 470
Db 487 GNTVQLRSLRLTYRNLSGDPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPILGAGRTPE 546
QY 471 GEEACGEHTPPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAM 530
Db 547 GEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRARA- 605
QY 531 AAAADKQGVGPGAGPLEGLGVKVPLEPGKATGEGGEALPSGECEVPLMGSPGLOS 590
Db 606 TSTAQDKGVGPGTGPLEGLGVKAPLEPGSKATGEGGEALSGGECEVPLMGYPGSLQ 665
QY 591 PLHAKPYI 598
Db 666 VLPKHYI 673

RESULT 3
VASN_XENTR
ID VASN_XENTR STANDARD; PRT; 661 AA.
AC Q6DFS5;
DT 18-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 16-AUG-2004, sequence version 1.
DT 30-MAY-2006, entry version 15.
DE Vasorin precursor.
GN Namesvasn;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RG NIH - Xenopus Gene Collection (XGC) project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as an inhibitor of TGF-beta signaling (By
similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
protein (Probable).
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC
CC
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CC EMBL; BC076888; AAH76888.1; -; mRNA.
DR UniGene; Str. 8462;
DR InterPro; IPR008985; ConA_like lec_gl.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR004583; LRR_C.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00560; LRR_1; 8.

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Db 6 PLSHILLQLLCCGSSRCHDCTCLPSNNIFCVQRNLIMYRGLPSTGKQLYVFQNKIN 65  
Qy 66 MLDASSFAGLPGIQLDLSONQIA----- 89  
Db 66 ILQQDFVELGEMLDLSONSISEIPDGVSPLSLHNLDSNNVITHIKDSFGLVN 125  
Qy 90 -----SLRPLRLLLDLSHNSLLALE 110  
Db 126 LERLYLSNIIQNIHPAFAEGLENNLELKLQGNQISVLPAQLPRLHLDLSYNSIPPLV 185  
Qy 111 PGILDTANVEALRLAGLGLQOLDEGLFSRLRLNHLHDLDVSDNQLRVPVIRGLRGLTRLR 170  
Db 186 AQDLQTPHLESKIAGLGLTSLDEELGSLVNLHVLDSVQNLVDIQTLSKSMGGSLN 245  
Qy 171 LAGNTRIAQLRPEDLAGLAALQDGLSVNLQALPGDLSGLPRLRLAAARNPFCVCP 230  
Db 246 LTCNP-LGSLKHEDFQNLVNLLELDLSNMLQGFEGFNLFPKLEKLTAAENPFCVCP 304  
Qy 231 LSWFGPWVRESHVTLASPEETRCHFPFPKAGRLLELDYADFCPATTTTATVPTTRPVV 290  
Db 305 LAWFFPAWLKDVRLVRLTEETRCHFPFPKAGRLLELDYADFCPATTTTATVPTTRPVV 364  
Qy 291 REPTALSSSLAPTWSLPTAPATAPSPPTAPPTVGPVQ-----OD-----CP 335  
Db 365 SRPKNSSTQLGTHIVVPAP-----PSDISSADADNFPVQTTAFPSRIMEDSEGEIMCP 420  
Qy 336 PSTCLNGGTCGLTRHHLACPEGTGLYCESQMGQTPSP-----VTPPPRS 388  
Db 421 PNICLNGGTCIFKSNQVIVCLCPSSNGVCEIQ-NEAMLPSPSVLSLETIVQPN-- 477  
Qy 389 LTLGIEPVSPSLRVGLQRYLQSSVQLRLTYRLNLGPDKRLVTLRLPASLAETVT 448  
Db 478 -TISHHITSTSLDLHRYIQ-TRHIGIRITYNSLQSDRPLQLSVPPSYPEYTLR 535  
Qy 449 QLRPNATYVCMVPLGGRVPEGEACEAHT---PPAVHSHNAPVQVQAREGNLPLLIAP 505  
Db 536 GLQPNSTYVCSPLGE-PVHASVACMEARTAGIPSSHEPSVDRTEPSSSLTPVW-- 592  
Qy 506 ALAAVLLAALAAVGAAYCYVRGRAMAAADKQVGFAGLEGVKVPLEFG---PK 561  
Db 593 AVAVMVVAIIAT-VVVISRRRRPKAPVMDLHE---TSPLEMEGVKTNPENGTHPK 646

## RESULT 5

Q503G2 BRARE PRELIMINARY; PRT; 643 AA.  
AC Q503G2;  
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.  
DT 13-JUN-2006, sequence version 1.  
DE Slit-like 2.  
GN Name=vaen;  
OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Singapore local strain; TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Jordan H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.H.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Query Match 29.6%; Score 927.5; DB 2; Length 643;  
Best Local Similarity 36.4%; Pred. No. 2.2e-44;  
Matches 224; Conservative 77; Mismatches 201; Indels 113; Gaps 14;  
Qy 46 VPRDVPDVTGLYFENGITMLDASSFAGLPGIQLDLSONQIA----- 89  
Db 1 MPRGLPSTGKQLYVFQNKINILQQDFVELGEMLDLSONSISEIPDGVSPLSLHNL 60  
Qy 90 -----S 90  
Db 61 DLSSNYITHISKDSFGLVNLRLYLSNIQNIHPAFAEGLENNLELKLQGNQISVLPA 120  
Qy 91 LRLPRLLLDLSHNSLLALEPGILDNTANVEALRLAGLGLQOLDEGLFSRLRLNHLHDVSD 150  
Db 121 LQLPRLHLDLSYNSIPPLVAQDLQTPHLESKIAGLGLTSLDEELGSLNHLHVLDSQ 180  
Qy 151 NQLRVPVPIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQDGLSVNLQALPGDLSG 210  
Db 181 NQLVDIQTLSKSMGGSLNHLTGNP-LGSLKHEDFQNLVNLLELDLSNMLQGFEGFN 239  
Qy 211 LFPRLRLAAARNPFCVCPDLSWFGPWVRESHVTLASPEETRCHFPFPKAGRLLELDYA 270  
Db 240 LFPKLEKLTAAENPFCVCPDLSWFGPWVRESHVTLASPEETRCHFPFPKAGRLLELDYA 299  
Qy 271 DFCGPATTTTATVPTTRPVREPTALSSSLAPTWSLPTAPATAPSPPTAPP-----TVG 326  
Db 300 DFCGPATTTTATVPTTRPVREPTALSSSLAPTWSLPTAPATAPSPPTAPP-----TVG 359  
Qy 327 FVQPPQD-----CPPSTCLNGGTCGLTRHHLACPEGTGLYCESQMGQTPSP 379

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Db 360 PSRIMEDSEGEIMCPPNICLNGGTCTFKSNGVIVCLCPSPMSGLYCEIQ-NEAMLPPPS 418
Qy 380 P-----VTPRRSLTLGIBVPSPTSLRVGLQRYOGSSVOLRLTYRNLSPGDKR 432
Db 419 PAVSLTIATVQPN---TTSHHITSTISLDLHRYIQ-TRPHIRGLRITYSLNSGPDRR 474
Qy 433 LVTLRLPASLAEYTVTLQRLPNATYSVCVMPILGCRVPGEAEACGEAHT---PPAVHSNHA 489
Db 475 PLQLSVPPSYPEYTLRGLQPNSTYSVCASPLGE-PVHASVSACMEARTAGIPSSHEPSV 533
Qy 490 PVTQAREGNLPLLIAPALAAVLLAALAAVGAACVVRGRAMAAAOQKQGVGPGAGPLEL 549
Db 534 DRTESSSLTPIVV-AVAVMVVAIIAT-VVVISRRRPKAPVMDLHE-----TSPLEM 586
Qy 550 EGVKVPLEPG-----PK 561
Db 587 EGVKTNPENGTLHPK 601

RESULT 6
ID Q4S068_TETNG PRELIMINARY; PRT; 962 AA.
AC Q4S068_
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE Chromosome 19 SCAP14535, whole genome shotgun sequence.
GN ORFNames=GSTENG00014497001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mucelli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Cattolico L., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Para G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RP [2]
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CAAB01014535; CAF97214.1; -; Genomic_DNA.
CC DR GO:0005634; C:nucleus; IEA.
CC DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC DR InterPro; IPR000742; EGF_3.
CC DR InterPro; IPR006209; EGF_like.
CC DR InterPro; IPR013032; EGF_like_reg.
CC DR InterPro; IPR003961; FN_III.
CC DR InterPro; IPR008957; FN_III-like.
CC DR InterPro; IPR001611; LRR.
CC DR InterPro; IPR000483; LRR_C.

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DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR005033; YEATS.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00560; LRR_1; 8.
DR Pfam; PF03366; YEATS; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00882; LRRCT; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS1037; YEATS; 1.
SQ SEQUENCE 962 AA; 106856 MW; 3EC2C9402AC80BF6 CRC64;

Query Match 29.2%; Score 914.5; DB 2; Length 962;
Best Local Similarity 38.0%; Pred. No. 1.8e-43;
Matches 222; Conservative 77; Mismatches 190; Indels 95; Gaps 18;

Qy 57 LYVFENGITMDASSFAGLPGQLQLDLSQNOIA---SLRLPRLLLDLSHNSLLALEPGI 113
Db 388 LYLHGNLIQSIHAEFEGLEMLELKLQGNQLSLPSLRPRLLLDLSNNIPSLGSPD 447
Qy 114 LDTANVEALRLAGLGLQQLDEGLFSLRLNLHLDVSDNQLERYPPVIR--GLRGLTLRL 171
Db 448 FQTPHLEALKIVSLGSLMSIGDELIAWRNLHLDISMNQLTEVPLAKQSLGLIKLSL 507
Qy 172 AGNTRIAQLRPEDLAGLAALQELDVNSLSQALPGDLSGLFPRRLRLIAAARNPNCVCP 231
Db 508 AGNP-LGDLVEDFEKLTSLOELDLGLNLQGFSPSFLMFPRLTQLTAAENPNCICPL 566
Qy 232 SWFGPWVRESHVTLASPEETRCHFPKNAKRLLELDYADFGCAPATTTATVPTTRPV 291
Db 567 AWPVWLKKEKKNLRRPEETRCHFPKNAKRLLELDYADFGCAPATTTATVPTTRPV 618
Qy 292 EPTALSSSLAPTWSLPTAPATEAPSPSTAP-----PTVGPVPQPD----- 333
Db 619 SPTGSPSTPVSTPTTPKMTYTAIPPPPPSEIILFSPKTPYPLPPEPTSPSTSEVE 678
Qy 334 ---CPPSTCLNGGTCHLGRHRLACLCEGFTGLYCESQMGQGTSPSPVTPTRPPR--- 387
Db 679 SHICPNICLNGGTCHFDPMGQSLCICLSGTSGLYCN-----VDIVDPKHPV 728
Qy 388 ---SLTLGIEP-----VSPTSLRVGLQRYOGSSVOLRLTYRNLSPGDKRLV 434
Db 729 TEATLAASSVPVQNDALISSQVSTSTILLDLQRFIE-TRPHIRGLRITYSLNSGPD 787
Qy 435 TLRLPASLAEYTVTLQRLPNATYSVCVMPILG-----GRVPEGEACGEAHT----- 480
Db 788 ILSVPASYPEYTLRGLKPNCTYSVCASPLGERSVLRANSVDTG--SCTEARTEGILMTS 845
Qy 481 PPAVHSNHAAPVTOAREGNLPLLIAPALAAVLLAALAAVGAACVVRGRAMAAAOQKQ 540
Db 846 SSATAPTPGPMT-----FTLILAVSALALVGLSVAGTVCVRK-RRKAKAMELEMA 898
Qy 541 GPGAGPLEGKVPKLEPGPKATEGGEALPSG-----SECEVPL 580
Db 899 PADSDPMDLDMKLGLENGANGT-----LPHKQAQINRCHTFL 936

RESULT 7
LRC24_HUMAN
ID LRC24_HUMAN STANDARD; PRT; 513 AA.
AC Q50LG9;
DT 04-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2005, sequence version 1.
DT 30-MAY-2006, entry version 10.
DE Leucine-rich repeat-containing protein 24 precursor.
GN Name=LRC24;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;

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RN NUCLEOTIDE SEQUENCE [MRNA].  
 RP TISSUE=Brain;  
 RA Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;  
 RT "Novel gene containing leucine rich repeat on human chromosome 8.";  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP TISSUE=Brain;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass membrane protein  
 (Potential).  
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
 domain.  
 CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
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 DR EMBL: AB178281; BAD97811.1; -; mRNA.  
 DR EMBL: BC111067; AA111068.1; -; mRNA.  
 DR UniGene: Hs.591399; -.  
 DR Ensembl: ENSG00000188270; Homo sapiens.  
 DR HGNC: HGNC:28947; LRRC24.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR013098; Ig\_I-set.  
 DR InterPro: IPR003599; Ig\_sub.  
 DR InterPro: IPR003598; Ig\_sub2.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_C.  
 DR InterPro: IPR000372; LRR\_Cys\_N.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF07679; I-set; 1.  
 DR Pfam: PF00560; LRR 1; 5.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00408; IGC2; 1.  
 DR SMART: SM00369; LRR\_TYP; 3.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00835; IG LIKE; 1.  
 KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;  
 Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 513 Leucine-rich repeat-containing protein  
 potential.  
 FT FTId=PRO\_0000231596.  
 FT TRANSMEM 406 426 Potential.  
 FT REPEAT 49 72 LRR 1.  
 FT REPEAT 73 96 LRR 2.  
 FT REPEAT 98 120 LRR 3.  
 FT REPEAT 122 144 LRR 4.

FT REPEAT 145 168 LRR 5.  
 FT REPEAT 170 192 LRR 6.  
 FT REPEAT 244 265 LRR 7.  
 FT DOMAIN 260 361 Ig-like C2-type.  
 FT COMPIAS 375 378 Poly-Pro.  
 FT COMPIAS 427 432 Poly-Arg.  
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 363 363 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 281 345 By similarity.  
 SQ SEQUENCE 513 AA; 55199 MW; 3770FA80D979CIDE CRC64;  
 Query Match 11.8%; Score 368.5; DB 1; Length 513;  
 Best Local Similarity 26.4%; Pred. No. 9.3e-13;  
 Matches 170; Conservative 63; Mismatches 217; Indels 195; Gaps 28;  
 QY 1 MCSRRVLLPLLLLLALPGVCGSCGSCQSQQTCTARQGTTPRDPVPPDVTGLVVF 60  
 DB 1 MALRAPALLPLLLLL-LPLRAAGCPAACRC-YSATVECGALRVRVPLGIPPGTQTLFLQ 58  
 QY 61 ENGITMIDASSFAGLPGQLQLDLSONQIASLRL-----PRLLLDLHNSLLALEPG-I 113  
 DB 59 DNNIARLEPCALAPLAALRRLYLNHNSLRALEAGAFRAQPRLELALTSNRLRLRSAGF 118  
 QY 114 LDTANVEALRLAGLQQLDEGLFSRLRNLDVSDNQLRVPVIRGLRGLTRLRLAG 173  
 DB 119 VGLAQLRVLLAGNQLARLLDFTFLPLRLQELHLOENSIE----- 159  
 QY 174 NTRIAQLRPEDLAGLAALQELSDVSNLSLQALPGDLGSLFPRRLRLAAARNPENCVCPLSW 233  
 DB 160 -----LLEDAQLAGLSALLDLISRNQLGTISREALQPLASQLVRLTENPWRCDCAHW 214  
 QY 234 FGPWVRESHVTLASPEETR--CHFPKKNAGRLLELDYADFGCPATTTATVPTTRPVVR 291  
 DB 215 LGAWIEGGQRLTSDRKIMCAEPFRALQSLLDVSHSLIC-----IPSVHV-- 264  
 QY 292 EPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPQDCPP--STCLNGTCHLGT 349  
 DB 265 QPLELTANLGED-LRVACQASGYPQ---LVTWRKVPQPREGRPRAQAQLEGGL--LGL 317  
 QY 350 RHHLACLCPGPF-----TGLY-CESQMGCG-----TRSP-TPVTRP 385  
 DB 318 GHSASDTGSGMLFSLNITLAHAGKYCEASNAGGAARVFRLLVNASROOQPOQPAQPPP 377  
 QY 386 PRSITIGIEPVSPTSLRVGLQRLVQSSVOLRLTYRNLGSDPKRLVTLRLPASLAEY 445  
 DB 378 PAARPAGSEP----- 387  
 QY 446 TVTQLRENATYSVCMPLGFRVPEGEACGEAHTPPAVHSHNAPVTQAREGNLPLLIAP 505  
 DB 388 -----REAG-SMAFRALG-----VATQT-----AIAA 409  
 QY 506 ALAAVLLAALAAVGAACVRRGRAMAAADKQGVGGA-----GP---LEEGVK- 553  
 DB 410 AIALLALTALLV-AMICRRRRRRKKA---RGPPGEGALFVNDYLDGCPCTFAQLEELRD 464  
 QY 554 -----VPLEPGPKATEGGEALPGSECEVEPLMGFPFGGLQSP 591  
 DB 465 ERGHEMFVNRKSLPFAEGPAEA---PADCG-PAQG-AGPGLRVP 504  
 RESULT 8  
 LRFN4 HUMAN  
 ID LRFN4\_HUMAN STANDARD; PRT; 635 AA.  
 AC Q6FUG9; Q9BMWJ0;  
 DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 05-JUL-2004, sequence version 1.  
 DT 13-JUN-2006, entry version 27.  
 DE Leucine-rich repeat and fibronectin type-III domain-containing protein  
 DE 4 precursor.  
 GN Name=LRFN4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;









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Qy 65 TMLDASSFAGLPGQLQLDLSQNOIASL-----RLPRLLLDLSHNSLLAL-EPGILDTA 117
Dy 61 QALGPPDFRNMTGLVDLTLSRNAITRIGARSGDLESLSLHDGNRLVELGSSSLRGPV 120
Qy 118 NVEALRLAGLQQLDEGLFSR-LRNLHLDVSDNQLERP-VPIRGLRGLTFLRLAGNT 175
Dy 121 NLQHLILSGNLQRIAPGAFDDFLDLSLEDVSYNNLRQVPWAGIGSMPALHTLNLHDNL 180
Qy 176 RIAQLRPEDLAGLAALQELDVNSLSQALPGDLSGLFPRLR-----LLAAARNPFN 226
Dy 181 -IDALPGVFAQLSRLDLSNRLATLAPD--PLFSRGRDAEASPSPLVLSFGSNPLH 237
Qy 227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPKKNAGRLLELDYADFGCPATTTATVPT 285
Dy 238 CNECLLWLR-----RLRPDDLETSCASPPTLAGRYFWAVPEGEFSC----- 278
Qy 286 TRPVVREPTALSSSLAPTWSLTAPAT---EAPSPSTAPPTVGPVPQPD----- 333
Dy 279 -----EPPLIARHTQRLWLEGQATLRCALGDPVPTMHWVG-----PDRDLVGNSSRA 328
Qy 334 -CPPSTCLNGGTCGLTRHHLACL-PEGFTGLYCESOM-----GQTRPSPTP 380
Dy 329 WAFPNGLTLEIGVTGAGDAGAYTCIATNPAGEATARVELRLVLPALPHGNTSAEGRGPSD 388
Qy 381 VTPRPPRSL-----TLGIEP---VSPTSRLVGLQRYLQSSVQ-LRSLRLTYRNLSPDKR 432
Dy 389 IAASARTAEGBGLESEPAVQTEVTATSGLVSGLGRPADVPMWFQIQYN--SSEDET 446
Qy 433 LVTLRLPASLAEYVTQLRPNATYSVCVMPLGPRVPEGEA-----CCEAHTPPAVHNS 487
Dy 447 LIYRIVPASSHHFLKHLVPGADYDLCILALSPAAGPSDLTATRLIGCAHFSTLPATPLC 506
Qy 488 HAPVTOAREGNPLLIAPALAAVLAALAAVGAAYCVRRGRAMAAADKQGVGPAGPL 547
Dy 507 HALQAHVLGGTLTV---AVGGVLVAALLVFTVALLV-RGRG-----AGNRLPL 551
Qy 548 ELEGVKVPLEPGKATEGGEALP 571
Dy 552 KLSHVQ-----SQTNGTSPMP 568

RESULT 10
Q460G5_MOUSE PRELIMINARY; PRT; 636 AA.
AC Q460G5_MOUSE
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-JUN-2006, entry version 8.
DE Synaptic adhesion-like molecule 3.
GN Name=Lrnf4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Wang C.-Y., Wenthold R.J.;
RT "Synaptic Adhesion-Like Molecules, a Novel Family of Proteins
RL Interacting with NMDA Receptor and MAGUKs.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; DQ078786; AAZ23615.1; -; mRNA.
DR MGI; MGI:2385612; Lrnf4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR013098; Ig_I-set.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR003598; Ig_sub2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF07679; I-set; 1.
DR Pfam; PF00560; LRR_1; 5.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; ICG2; 1.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS00835; IG LIKE; 1.
SQ SEQUENCE 636 AA; 67265 MW; 9CE86E8A3981A884 CRC64;

Query Match 11.1%; Score 348; DB 2; Length 636;
Best local similarity 27.2%; Pred. No. 1.7e-11;
Matches 170; Conservative 62; Mismatches 276; Indels 116; Gaps 25;

Qy 8 LPLLLLLALGPGVQCGPSGQC---SQPTVFCTARQGTTPRDPDPTVGLVVFNGI 64
Dy 1 MAPPLLLLLASAAACPLPCVCONLSESLTCAHRLGLFVPPNDRRTVELRLADNFI 60
Qy 65 TMLDASSFAGLPGQLQLDLSQNOIASL-----RLPRLLLDLSHNSLLAL-EPGILDTA 117
Dy 61 QALGPPDFRNMTGLVDLTLSRNAITRIGARSGDLESLSLHDGNRLVELGSSSLRGPV 120
Qy 118 NVEALRLAGLQQLDEGLFSR-LRNLHLDVSDNQLERP-VPIRGLRGLTFLRLAGNT 175
Dy 121 NLQHLILSGNLQRIAPGAFDDFLDLSLEDVSYNNLRQVPWAGIGSMPALHTLNLHDNL 180
Qy 176 RIAQLRPEDLAGLAALQELDVNSLSQALPGDLSGLFPRLR-----LLAAARNPFN 226
Dy 181 -IDALPGVFAQLSRLDLSNRLATLAPD--PLFSRGRDAEASPSPLVLSFGSNPLH 237
Qy 227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPKKNAGRLLELDYADFGCPATTTATVPT 285
Dy 238 CNECLLWLR-----RLRPDDLETSCASPPTLAGRYFWAVPEGEFSC----- 278
Qy 286 TRPVVREPTALSSSLAPTWSLTAPAT---EAPSPSTAPPTVGPVPQPD----- 333
Dy 279 -----EPPLIARHTQRLWLEGQATLRCALGDPVPTMHWVG-----PDRDLVGNSSRA 328
Qy 334 -CPPSTCLNGGTCGLTRHHLACL-PEGFTGLYCESOM-----GQTRPSPTP 380
Dy 329 WAFPNGLTLEIGVTGAGDAGAYTCIATNPAGEATARVELRLVLPALPHGNTSAEGRGPSD 388
Qy 381 VTPRPPRSL-----TLGIEP---VSPTSRLVGLQRYLQSSVQ-LRSLRLTYRNLSPDKR 432
Dy 389 IAASARTAEGBGLESEPAVQTEVTATSGLVSGLGRPADVPMWFQIQYN--SSEDET 446
Qy 433 LVTLRLPASLAEYVTQLRPNATYSVCVMPLGPRVPEGEA-----CCEAHTPPAVHNS 487
Dy 447 LIYRIVPASSHHFLKHLVPGADYDLCILALSPAAGPSDLTATRLIGCAHFSTLPANPLC 506
Qy 488 HAPVTOAREGNPLLIAPALAAVLAALAAVGAAYCVRRGRAMAAADKQGVGPAGPL 547
Dy 507 HALQAHVLGGTLTV---AVGGVLVAALLVFTVALLV-RGRG-----AGNRLPL 551
Qy 548 ELEGVKVPLEPGKATEGGEALP 571
Dy 552 KLSHVQ-----SQTNGTSPMP 568

RESULT 11
Q3UUS6_MOUSE PRELIMINARY; PRT; 634 AA.
ID Q3UUS6_MOUSE
AC Q3UUS6;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
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DT 18-APR-2006, entry version 8.  
DE 12 days embryo embryonic body between diaphragm region and neck cDNA,  
DE RIKEN full-length enriched library, clone:9430023110  
DE product:Fibronectin leucine rich transmembrane protein 2, full insert  
DE sequence.  
GN Name=Map4k5;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_TaxID=10090;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilmink L.G., Aidinis V., Allen J.E., Allen J.E.,  
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,  
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimonard S.M., Teasdale R.D., Liu E.T., Brusica V., Quackenbush J.,  
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
RN [4]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimonard S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.O., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Varadar R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staebli P., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RN [8]

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kicsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RA "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and  
RC neck;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AK136973; BAE23193.1; -; mRNA.  
DR MGI; MGI:1925503; Map4k5.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_C.  
DR InterPro; IPR000372; LRR\_Cys\_N.  
DR InterPro; IPR003591; LRR\_typ.  
DR InterPro; IPR013090; Phospholip\_A2\_AS.  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00560; LRR 1; 9.  
DR Pfam; PF01463; LRRCT; 1.  
DR Pfam; PF01462; LRRNT; 1.  
DR PRINTS; PRO0019; LEURICHRPT.  
DR SMART; SM00369; LRR\_TYP; 1.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00013; LRRNT; 1.  
DR PROSITE; PS00853; FN3; 1.  
DR PROSITE; PS00119; PA2\_ASP; UNKNOWN 1.  
KW Leucine-rich repeat; Membrane; Repeat; Transmembrane.  
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Query Match 10.9%; Score 341; DB 2; Length 634;  
Best Local Similarity 23.1%; Pred.No. 4.2e-11;  
Matches 143; Conservative 85; Mismatches 238; Indels 154; Gaps 19;  
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DB 11 RGAFILKFWLLISGLYLQVSKLLACPSVCRDR-NFVVCNERSLSVPLGIPEGTVVLY 69  
QY 59 VF-----  
DB 70 LHNQINNAGFAELHNVQS VHTVLYGNQLDEFPNLPKNVRLVHLQENNIQTISRAAL 129  
QY 73 AGLPGLQLDLSONQIASRLP-----RLLLDLSHNSLLALEPGI---LDTANVEA 121  
DB 130 AQLLKLEELHLDNDSISTVGVEDGAPFAISLKLFLSKNHLSSVPGVLPVLDLQELRVDE 189  
QY 122 LRLA---GLGLQOLD-----EGLFSRLRLNHLDDVSDNQLERVPVVI 160  
DB 190 NRIAVISDMAFQNLISLERLIYDGNLLTNKGTAEGTFSHTLKLERSIVNSLSHPDPL 249  
QY 161 RGLRLGLRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALGDLGSLFPRLRLAA 220  
DB 250 PGTH-LIRLYLDQN-QINHIPLTAFANRLKLERLDISNNQLRMLTQGVFDHLSNLQLTA 307

QY 221 ARNPENCVCPLSNFPGPMVRESHVHTLASPEETRCHFPKPNAGRLILLELDYADFGCPATTTT 280  
DB 308 RNNPWFCDGSIKWTEWLKIPSSL-NVRGFMCGPQVQVGMVARELNMLLSCTPTPG 366  
QY 281 ATVPTRPVVREPTALSSSLAPLWLSPTAPATEAPSPPTAPPTVGVPOQDCPPSTCL 340  
DB 367 LPVFTTAP-----STVSPITQSPTL-----SVPSPSRGSVPPAPTPSKLPTIPDW 411  
QY 341 NGGTCHLGTGRHHLACLCPGFTGLYCDSQMGQTRPSPTVTPPAPRPSLTILGIEFVSPTS 400  
DB 412 DG-----RERVTPPISERIQLSIHFNVDTS 436  
QY 401 LRVGLQRYLOGSSVOLRSRLTYRNLSPDKRLVTLRLPASLAEY-TVTLRNPATYSVC 459  
DB 437 IQVSWLSLFTVMAYKLTWVMQGHSLVGG-----IVQERIVSGEKQHSVLNLEPSTTRIC 492  
QY 460 VMLPGPRVPEGEA-CGEAHTPPA-----VHSNHPVTOQAREGNLPLLIAPALAAVL 511  
DB 493 LVPLDFAFNVRTVEDTTCSEATTHASYNLNGSNNTASHEQTTSMSG-S-PFLLAGLIGAV 551  
QY 512 LAALAAVGAAYC---VRRGR 528  
DB 552 IFVLVLLSVFVCFWHMKKGR 571  
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AC Q8BLJU0;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,  
DE clone: A530098L04 product: LUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN  
DE FLRT2 homolog (10 days neonate cerebellum cDNA, RIKEN full-length  
DE enriched library, clone: 6530421A03 product: Fibronectin leucine rich  
DE transmembrane protein 2, full insert sequence) (Fibronectin leucine  
DE rich transmembrane protein 2).  
GN Names: Flrt2; Synonyms: Map4k5;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilmom S.E., Aidinis V., Allen J.E.,  
RA Ambesi-Impombato A., Apweiler R., Attalaya R.N., Bono T., Bono H.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Gustincich S., Habbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,  
RA Rest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlesed C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watanishi A., Okamura-Ono Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).  
RL Science 309:1559-1563(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).  
RL Science 309:1564-1566(2005).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,  
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Offello T., Furuno M., Aono H., Baldarelli R., Barch G.,  
RA Blake J., Okazaki Y., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletchner C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).  
RL Nature 409:685-690(2001).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanishi A.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.  
RX 10 month old virgin mouse. Taken by biopsy.; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquelliano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S.C., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,

Query Match          10.9%; Score 341; DB 2; Length 660;
Best Local Similarity 23.1%; Pred. No. 4.4e-11;
Matches 143; Conservative 85; Mismatches 238; Indels 154; Gaps 19;

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QY 59 VF-----ENGINEMLDASSF 72
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QY 73 AGLPGQLLDLSONQIASRLP-----RLLLDLSHNSLLALEPGI---LDTANVEA 121
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QY 122 LRLA---GLGLQQLD-----EGLFSRLRLNHLDDVSDNQLERVPVPI 160
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QY 161 RGLRGTRLRAGNTRIARLPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLLRLAA 220
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DQ 250 PGTH-LIRLYLDQN-QINHIPLTAFANLRLERLDISNNQLRMLTQGVFDHLSNLKOLTA 307
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DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 341 NGGTCHLGTRHHLACIPGFTGLYCESQMGQGRPSPTVTPRPSRLTLGIEPVSPTS 400
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 412 DG-----RERVTPISERIQLSIHFVNDTS 436
QY 401 LRVGLQRYLOGSSVQLRSLRLTYRNLSPDKRLVTLRLPASLAEY-TVTLRPNATYSVC 459
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 437 IQVSMLSLFTVMAYKLTWVMGHSLVGG----IVQERIVSGEKOHLNVLNLEPRSTYRIC 492
QY 460 VMLPGRVPGEBEA-CGEAHTPPA-----VHSNHAPVTOAREGNLPLLIAPALAAVL 511
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 493 LVPDLAFNRTVETDTICSEATTHASYLNNGSNNTASSHEQTTSMSG-S-PFLLAGLIGGAV 551
QY 512 LAALAAGVGAAYC---VRRGR 528
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DQ 552 IFVLVLLSVFCWHHKKGR 571

RESULT 13
ID LRC24 MOUSE
AC Q8BHA1
DT 04-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 01-WAR-2003, sequence version 1.
DT 30-MAY-2006, entry version 3.
DE Leucine-rich repeat-containing protein 24 precursor.
GN Name=Lrc24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory bulb;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.B., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.D., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakamura H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Resole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiuira K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plesky C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayaehizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
CC
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CC
CC
CC ENBL; AK048678; BAC33419.1; -; mRNA.
CC ENBL; AK078176; BAC37163.1; -; mRNA.
CC UniGene; Mm.289666; -.
CC HSSP; Q9BZR6; LOZN.
CC Ensembl; ENSMUSG0000033707; Mus musculus.
CC MGI; MGI:3605040; Lrrc24.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR013098; Ig_I-set.
CC InterPro; IPR003598; Ig_sub.
CC InterPro; IPR003598; Ig_sub2.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_C.
CC InterPro; IPR003591; LRR_cyp.
CC Pfam; PF07679; I-set; 1.
CC Pfam; PF00560; LRR 1; 4.
CC Pfam; PF01463; LRRCT; 1.
CC PRINTS; PR00019; LEURICHRPT.
CC SMART; SM00409; IG; 1.
CC SMART; SM00408; IGC2; 1.
CC SMART; SM00369; LRR_TYP; 3.
CC SMART; SM00082; LRRCT; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
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KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;  
 KW Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 23 Potential.  
 FT CHAIN 24 521 Leucine-rich repeat-containing protein  
 FT 24  
 FT /FTId=PRO\_0000231597.  
 FT TRANSMEM 414 434 Potential.  
 FT REPEAT 57 80 LRR 1.  
 FT REPEAT 81 104 LRR 2.  
 FT REPEAT 106 128 LRR 3.  
 FT REPEAT 130 152 LRR 4.  
 FT REPEAT 153 176 LRR 5.  
 FT REPEAT 178 200 LRR 6.  
 FT REPEAT 252 273 LRR 7.  
 FT DOMAIN 268 371 Ig-like C2-type.  
 FT COMPIAS 435 440 Poly-Arg.  
 FT CARBOHYD 91 91 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 342 342 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 371 371 N-linked (GlcNAc... ) (Potential).  
 FT DISULFID 289 353 By similarity.  
 SQ SEQUENCE 521 AA; 56334 MW; 3D1E4BEE302284A6 CRC64;

Query Match 10.8%; Score 339; DB 1; Length 521;  
 Best Local Similarity 27.0%; Pred. No. 4.5e-11;  
 Matches 149; Conservative 66; Mismatches 217; Indels 120; Gaps 21;

Qy 1 MCSRVPFLLLPL---LLLLALPGCV---QCGPSGCCSQPQTVFCTARQGTTPRDPD 53  
 Db 1 MALRAPTLILLLLGLLLPLLPGLPRATGCPACRC-YSATVECGALRLRVPPGIPP 59  
 Qy 54 TVGLVVFENGITWLDASSFAGLPGQLDLDSQNIASLR-----LPRLLLDLSHNSLL 107  
 Db 60 TQTLPLQDMSIAHLEQGSAPLAALRHLYLHNNTLRALESAGFAQPRLLLELATGNRLR 119  
 Qy 108 ALEPG-ILDTANVEARLRLAGLQQLDEGLFSRLNHLHDVSDNQLERVPVIRGLRL 166  
 Db 120 GLRGGAFLVQLRVLYLAGNQLAKLLDFTFLHPLRLQLHLOENSTIE----- 167  
 Qy 167 TRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPF 226  
 Db 168 -----LLEQALAGLSLLALLDLSRNQLGTISKEALQPLSSLOVRLTENPWR 215  
 Qy 227 CVCPLSWFGPWRSHVTLASPETR--CHFFPKNAGRLLELDYADFQCPATTTATVP 284  
 Db 216 CDCALHWSWIKEGRRLLSSRDKKITCAEPRLALQSLLEVSGLSLC-----IP 267  
 Qy 285 TTRPVVREPTALSSLAPTWLSPTAPATEAPSPSPPTAPPTVGPVQPDCCP--STCLNG 342  
 Db 268 PSVNV--EPPEFTANLGED-LVACQASGYQPQ-----LVVWRKVPQPRDGKQQAQLE 320  
 Qy 343 GTCHLG-----TRHILACLPEGTGLY-CESQMGQGTSPPTPTVTPRPR 387  
 Db 321 GAPGLGGHTRDTGSMFLFNTITLA-----HAGKYECEAANAGGARVPFFHLVNASR 374  
 Qy 388 SLTLGI-EPVSPTSRLVGLQRYLQGSVQLRSRLTYRNLSPGDKRLVTL----- 436  
 Db 375 QSQQLPDPQAPATRPVGHPEQHEAGSMARFALCLATQTATTAIALLATALLAAMIC 434  
 Qy 437 -----RLPASLAEYV-----VTQLRPNATYSVCMV-----PLGPGRVPE 470  
 Db 435 RRRRRKKVPAPSGEGTLFVNDYSDGCTPQAELELDDHGHMFVDRSKPLPPEVL 493  
 Qy 471 GREACGEAHTPP 482  
 Db 494 -EEA--PEHNPP 502

RESULT 14  
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 ID Q4SGV9\_TETNG PRELIMINARY; PRT; 655 AA.  
 AC Q4SGV9;  
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.

DT 27-JUN-2006, entry version 8.  
 DE Chromosome 14 SCFA14590, whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTENG00018451001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciforma; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Micaudi E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
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 CC -----  
 CC EMBL: CAAE01014590; CAG00123.1; -; Genomic\_DNA.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_C.  
 DR InterPro; IPR000372; LRR\_Cys\_N.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00560; LRR\_1; 8.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF01462; LRRNT; 1.  
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 DR SMART; SM00369; LRR\_TYP; 1.  
 DR SMART; SM00082; LRRCT; 1.  
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 DR PROSITE; PS00853; FN3; 1.  
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Query Match 10.8%; Score 338; DB 2; Length 655;  
 Best Local Similarity 25.3%; Pred. No. 6.5e-11;  
 Matches 160; Conservative 78; Mismatches 206; Indels 188; Gaps 31;

Qy 7 LLLPLLLLLALGPGVQCGPSGCCSQPQTVFCTARQGTTPR----- 48  
 Db 13 LTVTLSLQVLRGGA-SCPOECRCDN-TFVYCNERSLTSVPLGQEGVKVLFLLNNQINN 70  
 Qy 49 -----DVPDPDTVGLVVFENGITMLDASSFAGLPGQL 80  
 Db 71 AGFPVELHLHLASVETVHLYGNQDLDEFFINLPKNTVFLQLQENNIQTISRALAQLTRLEE 130  
 Qy 81 LDLSQNIASLRPR-----LILLDLSHNSLLALEPGI---LDTANVEARLRLAGL- 128  
 Db 131 LHLDDNSTSTVGVEGAFREAVSLKLLFLTKNHLSSVPIGLPEELELRLDENRIAVIAE 190



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QY 129 -----LQQL-----DSGL-----PSRLNHLHDVSDNQLRVPVPPVIRGLGLTR 168
Db 191 EAFQNVTRLQRLLDGNLLTDEGIAGFTQDVLNRELALARNSLTFFPPPLFG-RALFR 249
QY 169 LRLAGNTRIAQLRPEDLAGLAQLQELDVNSLSIAL-QGLSGLFPRRLILAAARPENC 227
Db 250 LSLQEN-QIDQIPVAFAAGLHRLKLDVSSNQLSLQSGVFEGL-GALRHLVMVRNPNWRC 307
QY 228 VCPLSWFGPWVRESHVHTLASPEETR---CHFPKNAKGRILLLELDYADFGCPATTTATVP 284
Db 308 DCAVKVWVWLR---SLPASVNAFCVQSEKVGMAIRELTLDVIECP-----354
QY 285 TTRPVVRBETALSSSLAPTWSLPTAPATEAPSPSTAPPTVGVPOQPCPSTCLNGGT 344
Db 355 -----PGAGS-----PSW---PTLRST-PPPPPTAPTATTAGSTAITPP-----391
QY 345 CHLGRHHLACLCPGFTGLYCESQMGQTRSPST-----PVTPRPPRS---LTLGIEPVSP 398
Db 399 TSLRVLQRLYQSSVQLRSLRTV-----RNLSPDKRLVTLRLPASLAEVTVTLQRP 452
QY 431 SNIEVSWASYF-----TVTAYKVTVWVRGQGTNEGPRRTV-----GGQRRISLGNLEP 481
QY 453 NATYSVCVMPGLG-----PGRVPEGEACEAHTPPAVHS-----NHAPVTOAREG-NLP 500
Db 482 RSVYRICVHVLDLNSYRGE---DTLCSSEARTKAAASTKAPGRDHAP---QEGIHST 533
QY 501 LLIAPALAAVLLAALAAVGAAYC---VRRGRA 529
Db 534 LIMAGIIGGAVLLVLTLLGLFCWVYHRKSA 565

RESULT 15
Q6A073 MOUSE PRELIMINARY; PRT; 637 AA.
AC Q6A073,
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DE 27-JUN-2006, entry version 19.
DE MKIAA0405 protein (Fragment).
GN Name=Map4k5; Synonyms=Flrt2, mKIAA0405,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Muridae; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=1536895; DOI=10.1093/dnares/11.3.205;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT IV. The complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 11:205-218(2004).
CC
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CC -----
DR EMBL; AK172945; BAD32223.1; -; mRNA.
DR Ensembl; ENSMUSG0000047414; Mus musculus.
DR MGI; MGI:3603594; Flrt2
DR MGI; MGI:1925503; Map4k5,
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DR InterPro; IPR000372; LRR_Cys_N.
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DR Pfam; PF00560; LRR_1; 9.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00082; LRRCT; 1.
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Best Local Similarity 23.2%; Pred. No. 1.4e-10;
Matches 142; Conservative 81; Mismatches 233; Indels 156; Gaps 19;

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Db 3 LYLQVSKLLA-----CPSVCRCDR-NFYVCNERSLTSVPLGIEGVTVLVHLNNQINN 54
QY 61 -----ENCITWLDASSFAGLPGQL 80
Db 55 AGFPAELHNVSQVHTVYLYGNQLDEFPMLPKNVRVYLHQENNIQTISRALALQKLKEE 114
QY 81 LQLSONQIALSLP-----RLLLDLSHNSLLALEPGI---LDTANVEALRLA---G 126
Db 115 LHLDDNSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDQLRLVDENRIAVISD 174
QY 127 LGLQLQLD-----EGLFSRLNHLHDVSDNQLRVPVPPVIRGLGLTR 168
Db 175 MAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKKEFSIVRNSLSGHPDPDLPCTH-LIR 233
QY 169 IRLAGNTRIAQLRPEDLAGLAALQELDVNSLSIALQALPGDLISGLFPRLRLILAAARPENCV 228
Db 234 LYLQDN-QINHIPLTAPANLRKLERLDISNNQLRMLTQGVFDHLSNLKQLTARNNPMFCD 292
QY 229 CPLSWFGPWVRESHVHTLASPEETRCHFPKNAKGRILLLELDYADFGCPATTTATVPTRP 288
Db 293 CSIKWVTEWLKYPSSL-NVRGFMCGQPEQVGRMAVRELNMNLLSCPTTTPGLPVTTPAP 351
QY 289 VVREPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGVPOQPCDPPSPCLNGGTCHLG 348
Db 352 -----STVSPPTQSTPL-----SVPSRGSVPAPTPSKLPTIPDWG-----390
QY 349 TRHHLACLCEGFTGLYCESQMGQTRSPPTVTPRPRSLTLGIEPVSPTSIRVGLQRY 408
Db 391 -----RERVTPPISERIQLSIHFVNDTSIQVSWLSL 421
QY 409 LQSSVQLRSLRLTYRNLSPDKRLVTLRLPASLAEY-TVTQLRPNATYSVCVMPILGPGR 467
Db 422 FTMAYKLTWVMXGHSLVGG-----IVQERIVSGEKKOHLSLVNLNLEPRSTYRICVLDAFN 477
QY 468 VPEGEBA-CGEAHTPPA-----VHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVG 519
Db 478 YRTVEDTICSEATTTHASYLNNGSNASSHEQTTSMSG-S-PFLLAGLIGGAVIFVLVLL 536
QY 520 AAYC---VRRGR 528
Db 537 SVFCWHMHKKGR 548

Search completed: August 29, 2007, 08:55:28
Job time : 385 secs
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GenCore version 6.2.1.1  
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OM protein - protein search, using sw model

Run on: August 29, 2007, 08:49:40 ; Search time 309 Seconds  
 (without alignments)  
 1582.779 Million cell updates/sec

Perfect score: 3135  
 Sequence: 1 MCSRVPLLLPLLLALLGPG.....PLMGPPGGLQSLHAKPYI 598

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 352611 seqs, 817857308 residues

Total number of hits satisfying chosen parameters: 352611

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS2/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS2/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS2/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS2/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS2/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	ID	Description
3	3135	100.0	598 3	US-09-944-457-69 Sequence 69, Appl
70	3135	100.0	598 4	US-10-219-065-104 Sequence 104, Appl
121	3135	100.0	598 4	US-10-429-667-69 Sequence 69, Appl
126	3135	100.0	598 4	US-10-677-471-69 Sequence 69, Appl
127	3135	100.0	598 4	US-10-677-669-69 Sequence 69, Appl
129	3135	100.0	598 5	US-10-735-014-69 Sequence 69, Appl
130	3135	100.0	598 5	US-10-854-944-69 Sequence 69, Appl
131	3135	100.0	598 5	US-10-858-993-69 Sequence 69, Appl
133	3135	100.0	598 5	US-10-901-400-69 Sequence 69, Appl
134	3135	100.0	598 5	US-10-858-981-69 Sequence 69, Appl
135	3135	100.0	598 5	US-10-899-671-69 Sequence 69, Appl
136	3135	100.0	598 5	US-10-943-353-69 Sequence 69, Appl
142	3135	100.0	598 6	US-11-296-092-69 Sequence 69, Appl
143	3135	100.0	598 6	US-11-296-155-69 Sequence 69, Appl
145	3083.5	98.4	673 3	US-09-782-980-59 Sequence 59, Appl
171	3083.5	98.4	673 3	US-09-997-428-52 Sequence 52, Appl
366	3083.5	98.4	673 4	US-10-063-742-16 Sequence 16, Appl
367	3083.5	98.4	673 4	US-10-806-018-59 Sequence 59, Appl
368	3083.5	98.4	673 5	US-10-972-317-16 Sequence 16, Appl
370	3083.5	98.4	673 5	US-10-950-374-52 Sequence 52, Appl
371	3083.5	98.4	673 6	US-11-102-240-16 Sequence 16, Appl
372	3083.5	98.4	673 6	US-11-103-195-16 Sequence 16, Appl
373	3083.5	98.4	673 6	US-11-101-316-16 Sequence 16, Appl
374	3083.5	98.4	673 6	US-11-376-673-16 Sequence 16, Appl
375	3083.5	98.4	673 6	US-11-371-354-70967 Sequence 70967, A
376	3083.5	98.4	673 6	US-11-102-284-16 Sequence 16, Appl
377	3078.5	98.2	673 6	US-11-582-861-5594 Sequence 5594, Ap
			673 6	US-11-090-997-1750 Sequence 1750, Ap

378	3078.5	98.2	673	6	US-11-443-428A-840365	Sequence 840365,
379	3078.5	98.2	673	6	US-11-443-428A-840366	Sequence 840366,
380	3078.5	98.2	676	4	US-10-029-386-33083	Sequence 33083, A
381	2935	93.6	672	4	US-10-050-704-99	Sequence 99, Appl
382	2935	93.6	672	4	US-10-798-512-99	Sequence 99, Appl
383	2935	93.6	672	5	US-10-664-356-1475	Sequence 1475, Ap
384	2935	93.6	672	5	US-10-100-683-6220	Sequence 6220, Ap
385	2935	93.6	672	6	US-11-366-486-817	Sequence 817, App
386	2935	93.6	672	6	US-11-001-793-6220	Sequence 6220, Ap
387	2935	93.6	723	4	US-10-050-704-186	Sequence 186, App
388	2935	93.6	723	4	US-10-798-512-186	Sequence 186, App
389	2490	79.4	673	3	US-09-782-980-68	Sequence 68, Appl
390	2490	79.4	673	4	US-10-806-018-68	Sequence 68, Appl
391	2490	79.4	673	6	US-11-090-997-528	Sequence 528, App
392	2484	79.2	673	4	US-10-487-421-10	Sequence 10, Appl
393	2146.5	68.5	504	6	US-11-443-428A-840363	Sequence 840363,
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398	360.5	11.5	647	4	US-10-093-463-188	Sequence 188, App
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404	338	10.8	551	3	US-09-897-214-8	Sequence 8, Appl
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406	337	10.7	653	6	US-11-058-709-10	Sequence 10, Appl
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931	330	10.5	653	5	US-10-973-1158-438	Sequence 438, App
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SUMMARIES

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1	328.5	10.5	627	7	US-11-234-694-100 Sequence 100, App
2	261.5	8.3	347	7	US-11-627-164-2 Sequence 2, Appli
3	246	7.8	430	7	US-11-627-164-3 Sequence 3, Appli
4	244	7.8	708	6	US-10-533-069-849 Sequence 849, App
5	244	7.8	708	6	US-10-533-069-1942 Sequence 1942, App
6	240	7.7	560	6	US-10-533-069-2056 Sequence 2056, App
7	214.5	6.8	1094	6	US-10-533-069-2182 Sequence 2182, App
8	173.5	5.5	261	7	US-11-234-694-86 Sequence 86, Appl
9	158	5.0	363	7	US-11-649-663A-4510 Sequence 4510, App
10	154.5	4.9	514	7	US-11-649-663A-4386 Sequence 4386, App
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22	135	4.3	1473	6	US-10-438-246-16037 Sequence 16037, A
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136	96.5	3.1	842	6	US-10-438-246-20473	Sequence 20473, A	209	90	2.9	2246	6	US-10-438-246-25983	Sequence 25983, A
137	96	3.1	139	6	US-10-567-764-21	Sequence 21, Appl	210	90	2.9	2382	6	US-10-438-246-19285	Sequence 19285, A
138	96	3.1	525	6	US-10-438-246-31848	Sequence 31848, A	211	89.5	2.9	196	7	US-11-649-663A-3780	Sequence 3780, Ap
139	96	3.1	539	6	US-10-438-246-16737	Sequence 16737, A	212	89.5	2.9	535	7	US-11-649-663A-5542	Sequence 5542, Ap
140	96	3.1	539	6	US-10-438-246-24171	Sequence 24171, A	213	89.5	2.9	687	6	US-10-438-246-17592	Sequence 17592, A
141	95.5	3.0	577	7	US-11-649-663A-4440	Sequence 4440, Ap	214	89.5	2.9	687	6	US-10-438-246-24887	Sequence 24887, A
142	95.5	3.0	582	7	US-11-649-663A-5466	Sequence 5466, Ap	215	89.5	2.9	703	6	US-10-563-073-16	Sequence 16, Appl
143	95	3.0	636	7	US-11-656-389-52	Sequence 52, Appl	216	89.5	2.9	731	6	US-10-438-246-26301	Sequence 26301, A
144	95	3.0	1565	6	US-10-438-246-18794	Sequence 18794, A	217	89.5	2.9	872	6	US-10-533-069-64	Sequence 64, Appl
145	95	3.0	1565	6	US-10-438-246-25813	Sequence 25813, A	218	89.5	2.9	1189	7	US-11-691-348-613	Sequence 613, App
146	94.5	3.0	369	6	US-10-438-246-6290	Sequence 6290, Ap	219	89.5	2.9	1200	7	US-11-691-348-612	Sequence 612, App
147	94	3.0	470	6	US-10-438-246-17492	Sequence 17492, A	220	89.5	2.9	1407	7	US-11-691-348-628	Sequence 628, App
148	94	3.0	471	7	US-11-215-636A-42	Sequence 42, Appl	221	89.5	2.9	1449	6	US-10-438-246-18772	Sequence 18772, A
149	94	3.0	476	6	US-10-533-069-530	Sequence 530, App	222	89.5	2.9	1597	6	US-10-438-246-25811	Sequence 25811, A
150	94	3.0	522	6	US-10-533-069-302	Sequence 302, App	223	89.5	2.9	1670	6	US-10-438-246-16591	Sequence 16591, A
151	94	3.0	548	7	US-11-649-663A-3234	Sequence 3234, Ap	224	89.5	2.9	1785	6	US-10-438-246-18756	Sequence 18756, A
152	94	3.0	802	6	US-10-438-246-19279	Sequence 19279, A	225	89.5	2.9	2036	6	US-10-438-246-25352	Sequence 25352, A
153	94	3.0	1633	6	US-10-438-246-18850	Sequence 18850, A	226	89	2.8	348	6	US-10-438-246-18418	Sequence 18418, A
154	94	3.0	1851	6	US-10-438-246-20430	Sequence 20430, A	227	89	2.8	506	7	US-11-561-363-180	Sequence 180, App
155	93.5	3.0	108	6	US-10-567-764-17	Sequence 17, Appl	228	89	2.8	625	7	US-11-649-663A-4554	Sequence 4554, Ap
156	93.5	3.0	417	7	US-11-551-744-296	Sequence 296, App	229	89	2.8	651	6	US-10-438-246-18226	Sequence 18226, A
157	93.5	3.0	608	6	US-10-438-246-17214	Sequence 17214, A	230	89	2.8	680	6	US-10-438-246-25311	Sequence 25311, A
158	93	3.0	1815	6	US-10-438-246-18807	Sequence 18807, A	231	89	2.8	764	6	US-10-438-246-20470	Sequence 20470, A
159	93	3.0	2359	6	US-10-438-246-17328	Sequence 17328, A	232	89	2.8	1448	6	US-10-438-246-19310	Sequence 19310, A
160	93	3.0	2406	6	US-10-438-246-17330	Sequence 17330, A	233	89	2.8	1564	6	US-10-438-246-20614	Sequence 20614, A
161	92.5	3.0	327	6	US-10-533-069-775	Sequence 775, App	234	89	2.8	1578	6	US-10-438-246-25745	Sequence 25745, A
162	92.5	3.0	342	6	US-10-438-246-23590	Sequence 23590, A	235	89	2.8	1764	6	US-10-438-246-20380	Sequence 20380, A
163	92.5	3.0	393	7	US-11-649-663A-4406	Sequence 4406, Ap	236	89	2.8	1824	6	US-10-438-246-20444	Sequence 20444, A
164	92.5	3.0	726	6	US-10-438-246-19810	Sequence 19810, A	237	89	2.8	2493	6	US-10-438-246-26160	Sequence 26160, A
165	92.5	3.0	933	6	US-10-574-322-61	Sequence 61, Appl	238	89	2.8	2493	6	US-10-438-246-10762	Sequence 10762, A
166	92.5	3.0	1040	6	US-10-438-246-16103	Sequence 16103, A	239	88.5	2.8	162	6	US-10-438-246-5467	Sequence 5467, Ap
167	92.5	3.0	1239	7	US-11-561-363-34	Sequence 34, Appl	240	88.5	2.8	267	6	US-10-533-069-641	Sequence 641, App
168	92.5	3.0	1292	7	US-11-625-795-7	Sequence 7, Appli	241	88.5	2.8	389	7	US-11-649-663A-4816	Sequence 4816, Ap
169	92.5	3.0	1366	6	US-10-438-246-19694	Sequence 19694, A	242	88.5	2.8	455	6	US-10-438-246-18589	Sequence 18589, A
170	92.5	3.0	1573	6	US-10-438-246-16610	Sequence 16610, A	243	88.5	2.8	865	7	US-11-240-049-19	Sequence 19, Appl
171	92.5	3.0	1761	6	US-10-438-246-16288	Sequence 16288, A	244	88.5	2.8	1340	6	US-10-594-707-2	Sequence 2, Appli
172	92.5	3.0	1761	6	US-10-438-246-13874	Sequence 13874, A	245	88.5	2.8	1742	6	US-10-438-246-16114	Sequence 16114, A

246	88.5	2.8	2741	6	US-10-438-246-19335	Sequence 19335, A	319	86	2.7	413	6	US-10-438-246-8933	Sequence 8933, Ap
247	88.5	2.8	2742	6	US-10-438-246-25999	Sequence 25999, A	320	86	2.7	468	6	US-10-533-069-567	Sequence 567, App
248	88	2.8	471	6	US-10-438-246-16467	Sequence 16467, A	321	86	2.7	471	7	US-11-215-636A-44	Sequence 44, Appl
249	88	2.8	586	6	US-10-438-246-18162	Sequence 18162, A	322	86	2.7	472	6	US-10-438-246-9871	Sequence 9871, Ap
250	88	2.8	864	7	US-11-594-003-1	Sequence 1, Appli	323	86	2.7	530	7	US-11-215-636A-40	Sequence 40, Appl
251	88	2.8	864	7	US-11-594-003-3	Sequence 3, Appli	324	86	2.7	728	6	US-10-438-246-16256	Sequence 16256, A
252	88	2.8	864	7	US-11-594-003-4	Sequence 4, Appli	325	86	2.7	728	6	US-10-438-246-23852	Sequence 23852, A
253	88	2.8	864	7	US-11-594-003-5	Sequence 5, Appli	326	86	2.7	808	6	US-10-438-246-19033	Sequence 19033, A
254	88	2.8	864	7	US-11-594-003-7	Sequence 7, Appli	327	86	2.7	827	6	US-10-438-246-20733	Sequence 20733, A
255	88	2.8	1034	6	US-10-438-246-25951	Sequence 25951, A	328	86	2.7	847	6	US-10-438-246-18508	Sequence 18508, A
256	88	2.8	1205	6	US-10-438-246-25951	Sequence 25951, A	329	86	2.7	953	6	US-10-438-246-20157	Sequence 20157, A
257	88	2.8	1205	6	US-10-438-246-18183	Sequence 18183, A	330	86	2.7	1078	6	US-10-438-246-18855	Sequence 18855, A
258	88	2.8	1264	6	US-10-438-246-25280	Sequence 25280, A	331	86	2.7	1078	6	US-10-533-069-970	Sequence 970, App
259	88	2.8	1290	6	US-10-438-246-19448	Sequence 19448, A	332	86	2.7	1139	6	US-10-533-069-972	Sequence 972, App
260	88	2.8	1299	6	US-10-438-246-20063	Sequence 20063, A	333	86	2.7	1145	6	US-10-438-246-25760	Sequence 25760, A
261	88	2.8	1305	6	US-10-438-246-20063	Sequence 20064, A	334	86	2.7	1336	6	US-10-438-246-19547	Sequence 19547, A
262	88	2.8	1409	6	US-10-438-246-19273	Sequence 19273, A	335	86	2.7	1452	6	US-10-438-246-19547	Sequence 19547, A
263	88	2.8	1587	6	US-10-438-246-20075	Sequence 20075, A	336	86	2.7	1452	6	US-10-438-246-20042	Sequence 20042, A
264	88	2.8	1666	6	US-10-438-246-25661	Sequence 25661, A	337	86	2.7	1454	6	US-10-533-069-1144	Sequence 1144, Ap
265	88	2.8	1666	6	US-10-438-246-17333	Sequence 17333, A	338	86	2.7	1530	6	US-10-438-246-26184	Sequence 26184, A
266	88	2.8	1673	6	US-10-438-246-24678	Sequence 24678, A	339	86	2.7	1546	6	US-10-438-246-20069	Sequence 20069, A
267	88	2.8	1787	6	US-10-438-246-20125	Sequence 20125, A	340	86	2.7	1564	6	US-10-438-246-20046	Sequence 20046, A
268	88	2.8	1851	6	US-10-438-246-20415	Sequence 20415, A	341	86	2.7	1657	6	US-10-438-246-20395	Sequence 20395, A
269	88	2.8	2007	6	US-10-438-246-26167	Sequence 26167, A	342	86	2.7	1658	6	US-10-438-246-20395	Sequence 20395, A
270	87.5	2.8	335	6	US-10-438-246-25883	Sequence 25883, A	343	86	2.7	1732	6	US-10-438-246-26172	Sequence 26172, A
271	87.5	2.8	335	6	US-10-438-246-25570	Sequence 25570, A	344	86	2.7	1742	6	US-10-438-246-20118	Sequence 20118, A
272	87.5	2.8	402	6	US-10-533-069-851	Sequence 851, App	345	86	2.7	1743	6	US-10-438-246-20118	Sequence 20118, A
273	87.5	2.8	484	6	US-10-438-246-6083	Sequence 6083, Ap	346	86	2.7	1783	6	US-10-438-246-18831	Sequence 18831, A
274	87.5	2.8	530	6	US-10-438-246-16557	Sequence 16557, A	347	86	2.7	1963	6	US-10-438-246-20133	Sequence 20133, A
275	87.5	2.8	530	6	US-10-438-246-16557	Sequence 16557, A	348	86	2.7	1963	6	US-10-438-246-20133	Sequence 20133, A
276	87.5	2.8	608	6	US-10-438-246-24054	Sequence 24054, A	349	86	2.7	2264	6	US-10-438-246-25678	Sequence 25678, A
277	87.5	2.8	669	6	US-10-554-788-2	Sequence 2, Appli	350	86	2.7	2664	6	US-10-438-246-26222	Sequence 26222, A
278	87.5	2.8	713	6	US-10-438-246-18204	Sequence 18204, A	351	85.5	2.7	474	6	US-10-438-246-20118	Sequence 20118, A
279	87.5	2.8	1672	6	US-10-438-246-25676	Sequence 25676, A	352	85.5	2.7	575	7	US-11-650-478-2	Sequence 2, Appli
280	87.5	2.8	2511	6	US-10-438-246-10760	Sequence 10760, A	353	85.5	2.7	602	6	US-10-438-246-17739	Sequence 17739, A
281	87	2.8	170	6	US-10-438-246-25553	Sequence 25553, A	354	85.5	2.7	602	6	US-10-438-246-25033	Sequence 25033, A
282	87	2.8	301	6	US-10-438-246-8785	Sequence 8785, Ap	355	85.5	2.7	658	6	US-10-438-246-26244	Sequence 26244, A
283	87	2.8	340	6	US-10-438-246-5810	Sequence 5810, Ap	356	85.5	2.7	847	7	US-11-234-694-94	Sequence 94, Appl
284	87	2.8	659	6	US-10-438-246-19569	Sequence 19569, A	357	85.5	2.7	925	6	US-10-438-246-8418	Sequence 8418, Ap
285	87	2.8	685	6	US-10-438-246-5891	Sequence 5891, Ap	358	85.5	2.7	1012	6	US-10-533-069-60	Sequence 60, Appl
286	87	2.8	691	6	US-10-438-246-6041	Sequence 6041, Ap	359	85.5	2.7	1081	6	US-10-438-246-20393	Sequence 20393, A
287	87	2.8	709	6	US-10-438-246-17780	Sequence 17780, A	360	85.5	2.7	1240	6	US-10-438-246-19689	Sequence 19689, A
288	87	2.8	709	6	US-10-438-246-25013	Sequence 25013, A	361	85.5	2.7	1647	6	US-10-533-069-735	Sequence 735, App
289	87	2.8	999	6	US-10-438-246-20074	Sequence 20074, A	362	85.5	2.7	1742	6	US-10-438-246-25773	Sequence 25773, A
290	87	2.8	999	6	US-10-438-246-25680	Sequence 25680, A	363	85	2.7	179	6	US-10-438-246-5562	Sequence 5562, Ap
291	87	2.8	1253	6	US-10-438-246-20639	Sequence 20639, A	364	85	2.7	221	6	US-10-438-246-54207	Sequence 54207, A
292	87	2.8	1355	6	US-10-438-246-26261	Sequence 26261, A	365	85	2.7	245	7	US-11-561-363-74	Sequence 74, Appl
293	87	2.8	1475	6	US-10-438-246-20622	Sequence 20622, A	366	85	2.7	312	6	US-10-438-246-16010	Sequence 16010, A
294	87	2.8	1475	6	US-10-438-246-26259	Sequence 26259, A	367	85	2.7	380	7	US-11-551-744-298	Sequence 298, App
295	87	2.8	1570	6	US-10-438-246-18922	Sequence 18922, A	368	85	2.7	428	7	US-11-589-261-526	Sequence 526, App
296	87	2.8	1865	6	US-10-438-246-25815	Sequence 25815, A	369	85	2.7	437	7	US-11-589-261-383	Sequence 383, App
297	87	2.8	1865	6	US-10-438-246-20097	Sequence 20097, A	370	85	2.7	595	6	US-10-533-069-1992	Sequence 1992, Ap
298	87	2.8	1880	6	US-10-438-246-20122	Sequence 20122, A	371	85	2.7	607	7	US-11-561-363-134	Sequence 134, App
299	87	2.8	2420	6	US-10-438-246-26001	Sequence 26001, A	372	85	2.7	618	7	US-11-649-663A-4854	Sequence 4854, Ap
300	87	2.8	2483	6	US-10-438-246-19338	Sequence 19338, A	373	85	2.7	739	6	US-10-438-246-17823	Sequence 17823, A
301	86.5	2.8	320	7	US-11-649-663A-3740	Sequence 3740, Ap	374	85	2.7	909	6	US-10-438-246-19887	Sequence 19887, A
302	86.5	2.8	325	7	US-11-351-522A-14	Sequence 14, Appl	375	85	2.7	1177	6	US-10-438-246-20391	Sequence 20391, A
303	86.5	2.8	383	6	US-10-438-246-16478	Sequence 16478, A	376	85	2.7	1293	6	US-10-438-246-20051	Sequence 20051, A
304	86.5	2.8	383	6	US-10-438-246-24031	Sequence 24031, A	377	85	2.7	1293	6	US-10-438-246-25655	Sequence 25655, A
305	86.5	2.8	485	6	US-10-438-246-16942	Sequence 16942, A	378	85	2.7	1327	6	US-10-438-246-20297	Sequence 20297, A
306	86.5	2.8	485	6	US-10-438-246-24352	Sequence 24352, A	379	85	2.7	1532	6	US-10-438-246-20027	Sequence 20027, A
307	86.5	2.8	506	6	US-10-438-246-17821	Sequence 17821, A	380	85	2.7	1532	6	US-10-438-246-25642	Sequence 25642, A
308	86.5	2.8	598	7	US-11-351-522A-6	Sequence 6, Appli	381	85	2.7	1588	6	US-10-438-246-25751	Sequence 25751, A
309	86.5	2.8	598	7	US-11-351-522A-12	Sequence 12, Appli	382	85	2.7	1594	6	US-10-438-246-20642	Sequence 20642, A
310	86.5	2.8	795	6	US-10-438-246-16354	Sequence 16354, A	383	85	2.7	1598	6	US-10-438-246-26043	Sequence 26043, A
311	86.5	2.8	894	6	US-10-438-246-19064	Sequence 19064, A	384	85	2.7	1686	6	US-10-438-246-26304	Sequence 26304, A
312	86.5	2.8	1534	6	US-10-438-246-20141	Sequence 20141, A	385	85	2.7	1719	6	US-10-438-246-19785	Sequence 19785, A
313	86.5	2.8	1534	6	US-10-438-246-25647	Sequence 25647, A	386	85	2.7	1731	6	US-10-438-246-19888	Sequence 19888, A
314	86.5	2.8	1731	6	US-10-438-246-18774	Sequence 18774, A	387	85	2.7	1731	6	US-10-438-246-25634	Sequence 25634, A
315	86.5	2.8	2209	6	US-10-438-246-10765	Sequence 10765, A	388	85	2.7	1777	6	US-10-438-246-18749	Sequence 18749, A
316	86.5	2.8	2309	6	US-10-438-246-10765	Sequence 10765, A	389	85	2.7	1954	6	US-10-438-246-17622	Sequence 17622, A
317	86	2.7	341	7	US-11-649-663A-3548	Sequence 3548, Ap	390	85	2.7	1990	6	US-10-438-246-17623	Sequence 17623, A
318	86	2.7	392	6	US-10-438-246-16058	Sequence 16058, A	391	85	2.7	1990	6	US-10-438-246-24909	Sequence 24909, A

392	84.5	2.7	77	6	US-10-567-764-13	Sequence 13, Appl	465	83.5	2.7	1600	6	US-10-438-246-20154	Sequence 20154, A
393	84.5	2.7	192	6	US-10-438-246-25568	Sequence 25568, A	466	83.5	2.7	1691	6	US-10-438-246-25752	Sequence 25752, A
394	84.5	2.7	258	7	US-11-553-567-14	Sequence 14, Appl	467	83.5	2.7	1729	6	US-10-438-246-20644	Sequence 20644, A
395	84.5	2.7	456	6	US-10-438-246-9753	Sequence 9753, Ap	468	83.5	2.7	1829	6	US-10-438-246-25965	Sequence 25965, A
396	84.5	2.7	465	6	US-10-438-246-18606	Sequence 18606, A	469	83.5	2.7	2278	6	US-10-438-246-15860	Sequence 15860, A
397	84.5	2.7	465	6	US-10-438-246-25546	Sequence 25546, A	470	-83	2.6	310	6	US-10-438-246-19105	Sequence 19105, A
398	84.5	2.7	489	6	US-10-438-246-5486	Sequence 5486, Ap	471	83	2.6	316	7	US-11-649-663A-3124	Sequence 3124, Ap
399	84.5	2.7	560	6	US-10-593-213-6	Sequence 6, Appl	472	83	2.6	335	6	US-10-438-246-7939	Sequence 7939, Ap
400	84.5	2.7	596	6	US-10-438-246-18598	Sequence 18598, A	473	83	2.6	358	6	US-10-438-246-16304	Sequence 16304, A
401	84.5	2.7	886	6	US-10-438-246-17982	Sequence 17982, A	474	83	2.6	394	7	US-11-215-636A-26	Sequence 26, Appl
402	84.5	2.7	1073	6	US-10-438-246-20226	Sequence 20226, A	475	83	2.6	433	6	US-10-438-246-7547	Sequence 7547, Ap
403	84.5	2.7	1411	6	US-10-438-246-18771	Sequence 18771, A	476	83	2.6	493	6	US-10-438-246-31842	Sequence 31842, A
404	84.5	2.7	1473	6	US-10-438-246-20593	Sequence 20593, A	477	83	2.6	511	7	US-11-649-663A-5176	Sequence 5176, Ap
405	84.5	2.7	1473	6	US-10-438-246-25744	Sequence 25744, A	478	83	2.6	604	6	US-10-438-246-32712	Sequence 32712, A
406	84.5	2.7	1523	6	US-10-438-246-25744	Sequence 25744, A	479	83	2.6	684	6	US-10-438-246-17826	Sequence 17826, A
407	84.5	2.7	1632	6	US-10-438-246-26005	Sequence 26024, A	480	83	2.6	684	6	US-10-438-246-25045	Sequence 25045, A
408	84.5	2.7	1799	6	US-10-438-246-26005	Sequence 26005, A	481	83	2.6	729	6	US-10-438-246-20129	Sequence 20129, A
409	84.5	2.7	1825	6	US-10-438-246-20424	Sequence 20424, A	482	83	2.6	729	7	US-11-342-364-21	Sequence 21, Appl
410	84.5	2.7	1825	6	US-10-438-246-18815	Sequence 18815, A	483	83	2.6	729	7	US-11-342-364-22	Sequence 22, Appl
411	84.5	2.7	1825	6	US-10-438-246-25820	Sequence 25820, A	484	83	2.6	729	7	US-11-342-364-15	Sequence 15, Appl
412	84.5	2.7	1827	6	US-10-438-246-18739	Sequence 18739, A	485	83	2.6	813	7	US-11-342-364-17	Sequence 17, Appl
413	84.5	2.7	1827	6	US-10-438-246-25812	Sequence 25812, A	486	83	2.6	825	7	US-11-342-364-14	Sequence 14, Appl
414	84.5	2.7	1829	6	US-10-438-246-19233	Sequence 19233, A	487	83	2.6	841	6	US-10-438-246-19020	Sequence 19020, A
415	84.5	2.7	1848	6	US-10-438-246-19233	Sequence 19233, A	488	83	2.6	875	7	US-11-342-364-13	Sequence 13, Appl
416	84.5	2.7	1848	6	US-10-438-246-20417	Sequence 20417, A	489	83	2.6	976	6	US-10-438-246-20044	Sequence 20044, A
417	84.5	2.7	1851	6	US-10-438-246-20403	Sequence 20403, A	490	83	2.6	1016	7	US-11-342-364-18	Sequence 18, Appl
418	84.5	2.7	1851	6	US-10-438-246-20420	Sequence 20420, A	491	83	2.6	1022	7	US-11-342-364-17	Sequence 17, Appl
419	84	2.7	1851	6	US-10-438-246-26182	Sequence 26182, A	492	83	2.6	1116	6	US-10-438-246-16782	Sequence 16782, A
420	84	2.7	308	7	US-11-553-567-12	Sequence 12, Appl	493	83	2.6	1116	6	US-10-438-246-24229	Sequence 24229, A
421	84	2.7	321	6	US-10-438-246-16060	Sequence 16060, A	494	83	2.6	1154	6	US-10-438-246-24229	Sequence 24229, A
422	84	2.7	321	6	US-10-438-246-23807	Sequence 23807, A	495	83	2.6	1232	6	US-10-438-246-19768	Sequence 19768, A
423	84	2.7	360	6	US-10-438-246-6084	Sequence 6084, Ap	496	83	2.6	1357	6	US-10-438-246-18851	Sequence 18851, A
424	84	2.7	386	6	US-10-438-246-16697	Sequence 16697, A	497	83	2.6	1473	6	US-10-533-069-938	Sequence 938, App
425	84	2.7	386	6	US-10-438-246-24140	Sequence 24140, A	498	83	2.6	1563	6	US-10-438-246-15806	Sequence 15806, A
426	84	2.7	412	6	US-10-533-069-1813	Sequence 1813, Ap	499	83	2.6	1575	6	US-10-438-246-20080	Sequence 20080, A
427	84	2.7	466	7	US-11-213-575-70	Sequence 70, Appl	500	83	2.6	1666	6	US-10-438-246-26150	Sequence 26150, A
428	84	2.7	466	7	US-11-213-575-86	Sequence 86, Appl	501	83	2.6	1666	6	US-10-438-246-19790	Sequence 19790, A
429	84	2.7	471	6	US-10-438-246-17208	Sequence 17208, A	502	83	2.6	1690	6	US-10-438-246-26306	Sequence 26306, A
430	84	2.7	471	6	US-10-438-246-24619	Sequence 24619, A	503	83	2.6	1694	6	US-10-438-246-20402	Sequence 20402, A
431	84	2.7	512	6	US-10-438-246-9717	Sequence 9717, Ap	504	83	2.6	1694	6	US-10-438-246-26166	Sequence 26166, A
432	84	2.7	605	7	US-11-561-363-76	Sequence 33476, A	505	83	2.6	1720	6	US-10-438-246-20070	Sequence 20070, A
433	84	2.7	744	6	US-10-438-246-20035	Sequence 76, Appl	506	83	2.6	1730	6	US-10-438-246-20128	Sequence 20128, A
434	84	2.7	744	6	US-10-438-246-25646	Sequence 20035, A	507	83	2.6	1754	6	US-10-438-246-20128	Sequence 20053, A
435	84	2.7	746	6	US-10-438-246-19878	Sequence 25646, A	508	83	2.6	1820	6	US-10-438-246-20616	Sequence 20616, A
436	84	2.7	766	6	US-10-438-246-20055	Sequence 19878, A	509	83	2.6	2024	6	US-10-438-246-19129	Sequence 19129, A
437	84	2.7	806	6	US-10-438-246-20055	Sequence 20055, A	510	83	2.6	2155	6	US-10-438-246-19129	Sequence 20094, A
438	84	2.7	1079	6	US-10-438-246-9599	Sequence 9599, Ap	511	83	2.6	2155	6	US-10-438-246-25651	Sequence 25651, A
439	84	2.7	1406	6	US-10-438-246-8249	Sequence 8249, Ap	512	83	2.6	3330	6	US-10-438-246-16631	Sequence 16631, A
440	84	2.7	1488	6	US-10-438-246-25684	Sequence 25684, A	513	82.5	2.6	347	6	US-10-533-069-1946	Sequence 1946, Ap
441	84	2.7	1656	6	US-10-438-246-20123	Sequence 20123, A	514	82.5	2.6	359	6	US-10-533-069-1946	Sequence 229, App
442	84	2.7	1696	6	US-10-438-246-20090	Sequence 20090, A	515	82.5	2.6	372	7	US-11-551-744-299	Sequence 229, App
443	84	2.7	1747	6	US-10-438-246-25233	Sequence 25233, A	516	82.5	2.6	418	6	US-10-533-069-1168	Sequence 1168, Ap
444	84	2.7	1760	6	US-10-438-246-18831	Sequence 18831, A	517	82.5	2.6	466	6	US-10-438-246-18641	Sequence 18641, A
445	84	2.7	1882	6	US-10-438-246-18093	Sequence 18093, A	518	82.5	2.6	543	6	US-10-533-069-254	Sequence 254, App
446	84	2.7	2614	6	US-10-438-246-19225	Sequence 19093, A	519	82.5	2.6	596	6	US-10-438-246-25539	Sequence 25539, A
447	83.5	2.7	255	6	US-10-533-069-1142	Sequence 19225, Ap	520	82.5	2.6	698	6	US-10-438-246-30383	Sequence 30383, A
448	83.5	2.7	503	7	US-11-649-663A-3230	Sequence 1142, Ap	521	82.5	2.6	977	6	US-10-438-246-25168	Sequence 25168, A
449	83.5	2.7	504	7	US-11-649-663A-4058	Sequence 3230, Ap	522	82.5	2.6	1297	7	US-11-551-744-222	Sequence 222, App
450	83.5	2.7	584	7	US-11-649-663A-4312	Sequence 4312, Ap	523	82.5	2.6	1484	6	US-10-438-246-23668	Sequence 23668, A
451	83.5	2.7	642	7	US-11-629-727-48	Sequence 48, Appl	524	82.5	2.6	1567	6	US-10-438-246-19450	Sequence 19450, A
452	83.5	2.7	660	6	US-10-438-246-19992	Sequence 19992, A	525	82.5	2.6	1605	6	US-10-438-246-18830	Sequence 18830, A
453	83.5	2.7	671	6	US-10-438-246-17734	Sequence 17734, A	526	82.5	2.6	1606	6	US-10-438-246-25805	Sequence 25805, A
454	83.5	2.7	702	6	US-10-438-246-17235	Sequence 17235, A	527	82.5	2.6	1659	6	US-10-438-246-15988	Sequence 15998, A
455	83.5	2.7	719	6	US-10-438-246-24637	Sequence 24637, A	528	82.5	2.6	1680	6	US-10-438-246-20084	Sequence 20084, A
456	83.5	2.7	738	6	US-10-438-246-25667	Sequence 25667, A	529	82.5	2.6	1767	6	US-10-438-246-19172	Sequence 19172, A
457	83.5	2.7	789	6	US-10-438-246-25629	Sequence 25629, A	530	82.5	2.6	1848	6	US-10-438-246-25659	Sequence 25659, A
458	83.5	2.7	836	6	US-10-438-246-16854	Sequence 26293, A	531	82.5	2.6	1884	6	US-10-438-246-20082	Sequence 20082, A
459	83.5	2.7	836	6	US-10-438-246-24373	Sequence 16854, A	532	82	2.6	131	7	US-11-594-003-11	Sequence 11, Appl
460	83.5	2.7	1074	6	US-10-438-246-18928	Sequence 24373, A	533	82	2.6	233	6	US-10-438-246-25384	Sequence 25384, A
461	83.5	2.7	1462	7	US-11-649-663A-542	Sequence 18928, A	534	82	2.6	290	6	US-10-438-246-7550	Sequence 7550, Ap
462	83.5	2.7	1470	6	US-10-438-246-25859	Sequence 542, App	535	82	2.6	354	6	US-10-438-246-25574	Sequence 25574, A
463	83.5	2.7	1513	6	US-10-438-246-26036	Sequence 25859, A	536	82	2.6	494	6	US-10-438-246-24276	Sequence 24276, A
464	83.5	2.7	1566	6	US-10-438-246-20034	Sequence 26036, A	537	82	2.6	497	6	US-10-438-246-33376	Sequence 33376, A

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539	82	2.6	590	6	US-10-438-246-23902	Sequence 23902, A	612	80.5	2.6	336	6	US-10-438-246-8879	Sequence 8879, Ap
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541	82	2.6	657	6	US-10-438-246-15913	Sequence 15913, A	614	80.5	2.6	440	6	US-10-438-246-24898	Sequence 24898, Ap
542	82	2.6	657	6	US-10-438-246-23625	Sequence 23625, A	615	80.5	2.6	485	6	US-10-438-246-8890	Sequence 24808, A
543	82	2.6	803	6	US-10-438-246-26234	Sequence 26234, A	616	80.5	2.6	502	6	US-10-438-246-18498	Sequence 18498, A
544	82	2.6	835	6	US-10-438-246-5973	Sequence 5973, Ap	617	80.5	2.6	502	6	US-10-438-246-25461	Sequence 25461, A
545	82	2.6	872	6	US-10-438-246-20250	Sequence 20250, A	618	80.5	2.6	532	6	US-10-438-246-17449	Sequence 17449, A
546	82	2.6	881	6	US-10-438-246-18859	Sequence 18859, A	619	80.5	2.6	537	6	US-10-438-246-24868	Sequence 24868, A
547	82	2.6	1015	6	US-10-533-069-1017	Sequence 1017, Ap	620	80.5	2.6	642	6	US-10-438-246-18252	Sequence 18252, A
548	82	2.6	1156	6	US-10-438-246-19290	Sequence 19290, A	621	80.5	2.6	665	6	US-10-533-069-2369	Sequence 2369, Ap
549	82	2.6	1200	6	US-10-438-246-25982	Sequence 25982, A	622	80.5	2.6	713	6	US-10-438-246-20007	Sequence 20007, A
550	82	2.6	1532	6	US-10-438-246-16601	Sequence 16601, A	623	80.5	2.6	798	7	US-11-725-235-66	Sequence 66, Appl1
551	82	2.6	1537	6	US-10-438-246-18864	Sequence 18864, A	624	80.5	2.6	1133	6	US-10-438-246-18727	Sequence 18727, A
552	82	2.6	1562	6	US-10-438-246-20422	Sequence 20422, A	625	80.5	2.6	1459	7	US-11-649-663A-1332	Sequence 1332, Ap
553	82	2.6	1562	6	US-10-438-246-20427	Sequence 20437, A	626	80.5	2.6	1494	6	US-10-438-246-26291	Sequence 26291, A
554	82	2.6	1595	6	US-10-438-246-26178	Sequence 26178, A	627	80.5	2.6	1559	6	US-10-438-246-19214	Sequence 19214, A
555	82	2.6	1620	6	US-10-438-246-20438	Sequence 20438, A	628	80.5	2.6	1561	6	US-10-438-246-18773	Sequence 18773, A
556	82	2.6	1621	6	US-10-438-246-26181	Sequence 26181, A	629	80.5	2.6	1680	7	US-10-438-246-26177	Sequence 26177, A
557	82	2.6	1654	6	US-10-438-246-10484	Sequence 10484, A	630	80.5	2.6	1693	7	US-11-249-182-53	Sequence 53, Appl1
558	82	2.6	1676	6	US-10-438-246-25831	Sequence 25831, A	631	80.5	2.6	1721	6	US-10-438-246-25652	Sequence 25652, A
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563	82	2.6	2003	6	US-10-438-246-25687	Sequence 25687, A	636	80.5	2.6	4245	6	US-10-438-246-17856	Sequence 17856, A
564	82	2.6	2011	6	US-10-438-246-20093	Sequence 20093, A	637	80	2.6	218	6	US-10-438-246-18272	Sequence 18272, A
565	82	2.6	2174	6	US-10-438-246-19842	Sequence 19842, A	638	80	2.6	246	6	US-10-438-246-18201	Sequence 18201, A
566	82	2.6	2623	6	US-10-438-246-19875	Sequence 19875, A	639	80	2.6	295	6	US-10-438-246-33366	Sequence 33366, A
567	81.5	2.6	126	7	US-11-594-003-13	Sequence 13, Appl1	640	80	2.6	340	7	US-11-649-663A-3970	Sequence 3970, Ap
568	81.5	2.6	216	7	US-11-649-663A-5010	Sequence 5010, Ap	641	80	2.6	373	6	US-10-438-246-17447	Sequence 17447, A
569	81.5	2.6	277	7	US-11-551-744-300	Sequence 300, App	642	80	2.6	373	6	US-10-438-246-24858	Sequence 24858, A
570	81.5	2.6	359	6	US-10-438-246-7976	Sequence 7976, Ap	643	80	2.6	401	6	US-10-438-246-25302	Sequence 25302, A
571	81.5	2.6	377	6	US-10-438-246-16049	Sequence 16049, A	644	80	2.6	449	7	US-11-649-663A-3678	Sequence 3678, Ap
572	81.5	2.6	377	6	US-10-438-246-23804	Sequence 23804, A	645	80	2.6	484	6	US-10-438-246-33364	Sequence 33364, A
573	81.5	2.6	405	6	US-10-438-246-8896	Sequence 8896, Ap	646	80	2.6	495	6	US-10-438-246-8280	Sequence 8280, Ap
574	81.5	2.6	502	6	US-10-438-246-18081	Sequence 18081, A	647	80	2.6	512	7	US-11-234-694-110	Sequence 110, App
575	81.5	2.6	548	6	US-10-438-246-19654	Sequence 19654, A	648	80	2.6	519	6	US-10-438-246-5632	Sequence 5622, Ap
576	81.5	2.6	575	6	US-10-438-246-18485	Sequence 18485, A	649	80	2.6	645	6	US-10-438-246-18466	Sequence 18466, A
577	81.5	2.6	1455	6	US-10-438-246-19996	Sequence 19996, A	650	80	2.6	645	6	US-10-438-246-25405	Sequence 25405, A
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580	81.5	2.6	1736	6	US-10-438-246-26164	Sequence 26164, A	653	80	2.6	936	6	US-10-438-246-25685	Sequence 25685, A
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582	81.5	2.6	1784	6	US-10-438-246-18816	Sequence 18816, A	655	80	2.6	1050	6	US-10-438-246-25891	Sequence 25891, A
583	81.5	2.6	1784	6	US-10-438-246-25818	Sequence 25818, A	656	80	2.6	1134	7	US-11-649-663A-2104	Sequence 2104, Ap
584	81.5	2.6	1882	6	US-10-438-246-20029	Sequence 20029, A	657	80	2.6	1134	7	US-11-649-663A-2248	Sequence 2248, Ap
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587	81	2.6	475	7	US-11-649-663A-3800	Sequence 3800, Ap	660	80	2.6	1431	7	US-11-649-663A-1000	Sequence 1000, Ap
588	81	2.6	562	7	US-11-489-234-5	Sequence 5, Appl1	661	80	2.6	1491	6	US-10-438-246-20089	Sequence 20089, A
589	81	2.6	722	6	US-10-438-246-16501	Sequence 16501, A	662	80	2.6	1536	6	US-10-438-246-20032	Sequence 20032, A
590	81	2.6	744	6	US-10-438-246-20045	Sequence 20045, A	663	80	2.6	1542	6	US-11-656-389-6	Sequence 6, Appl1
591	81	2.6	944	6	US-10-438-246-17786	Sequence 17786, A	664	80	2.6	1585	7	US-11-656-389-6	Sequence 19250, A
592	81	2.6	944	6	US-10-438-246-25014	Sequence 25014, A	665	80	2.6	1636	6	US-10-438-246-19252	Sequence 19252, A
593	81	2.6	1220	7	US-11-649-663A-1542	Sequence 1542, Ap	666	80	2.6	1636	6	US-10-438-246-25968	Sequence 25968, A
594	81	2.6	1253	6	US-10-438-246-19539	Sequence 19539, A	667	80	2.6	1636	6	US-10-438-246-20060	Sequence 20060, A
595	81	2.6	1267	6	US-10-438-246-20092	Sequence 20092, A	668	80	2.6	1693	6	US-10-438-246-20060	Sequence 25671, A
596	81	2.6	1298	6	US-10-438-246-25681	Sequence 25681, A	669	80	2.6	1693	6	US-10-438-246-25671	Sequence 20054, A
597	81	2.6	1371	6	US-10-533-069-1037	Sequence 1037, Ap	670	80	2.6	1709	6	US-10-438-246-20054	Sequence 20104, A
598	81	2.6	1398	6	US-10-438-246-18788	Sequence 18788, A	671	80	2.6	1779	6	US-10-438-246-20104	Sequence 20104, A
599	81	2.6	1429	7	US-11-649-663A-2274	Sequence 2274, Ap	672	80	2.6	1822	6	US-10-438-246-26165	Sequence 26165, A
600	81	2.6	1634	6	US-10-438-246-20155	Sequence 20155, A	673	80	2.6	1827	6	US-10-438-246-25848	Sequence 25848, A
601	81	2.6	1634	6	US-10-438-246-25654	Sequence 25654, A	674	79.5	2.5	227	6	US-10-438-246-5641	Sequence 5641, Ap
602	81	2.6	1667	6	US-10-438-246-10527	Sequence 10527, A	675	79.5	2.5	260	6	US-10-438-246-24552	Sequence 24652, A
603	81	2.6	1802	6	US-10-438-246-18810	Sequence 18810, A	676	79.5	2.5	314	7	US-11-649-663A-3352	Sequence 3352, Ap
604	81	2.6	1802	6	US-10-438-246-25787	Sequence 25787, A	677	79.5	2.5	315	7	US-11-725-235-84	Sequence 84, Appl1
605	81	2.6	1851	6	US-10-438-246-20470	Sequence 20470, A	678	79.5	2.5	315	7	US-11-649-663A-224	Sequence 224, App
606	81	2.6	1855	6	US-10-438-246-25803	Sequence 25803, A	679	79.5	2.5	330	7	US-11-691-348-322	Sequence 322, App
607	81	2.6	1864	6	US-10-438-246-25803	Sequence 25803, A	680	79.5	2.5	392	7	US-11-649-663A-3370	Sequence 3370, Ap
608	81	2.6	2020	6	US-10-438-246-19035	Sequence 19035, A	681	79.5	2.5	426	6	US-10-438-246-15914	Sequence 15914, A
609	80.5	2.6	219	6	US-10-438-246-20640	Sequence 20640, A	682	79.5	2.5	426	6	US-10-438-246-23628	Sequence 23628, A
610	80.5	2.6	222	6	US-10-438-246-23889	Sequence 23889, A	683	79.5	2.5	442	6	US-10-438-246-16540	Sequence 16540, A
					Sequence 16681, A								

684	79.5	2.5	693	6	US-10-438-246-16017	Sequence 16017, A	757	78.5	2.5	1132	7	US-11-691-348-344	Sequence 344, App
685	79.5	2.5	739	6	US-10-533-069-22114	Sequence 22114, Ap	758	78.5	2.5	1134	7	US-11-691-348-611	Sequence 611, App
686	79.5	2.5	791	6	US-10-438-246-18832	Sequence 18832, A	759	78.5	2.5	1157	6	US-10-438-246-18789	Sequence 18789, A
687	79.5	2.5	1014	7	US-11-071-761-4	Sequence 4, Appli	760	78.5	2.5	1322	6	US-10-438-246-26098	Sequence 26098, A
688	79.5	2.5	1014	7	US-11-071-761-139	Sequence 139, App	761	78.5	2.5	1382	6	US-10-438-246-20389	Sequence 20389, A
689	79.5	2.5	1192	6	US-10-438-246-18786	Sequence 18786, A	762	78.5	2.5	1382	6	US-10-438-246-26176	Sequence 26176, A
690	79.5	2.5	1202	6	US-10-438-246-25804	Sequence 25804, A	763	78.5	2.5	1389	7	US-11-730-071-6	Sequence 6, Appli
691	79.5	2.5	1441	6	US-10-438-246-26264	Sequence 26264, A	764	78.5	2.5	1475	6	US-10-438-246-25709	Sequence 25709, A
692	79.5	2.5	1454	6	US-10-438-246-19767	Sequence 19767, A	765	78.5	2.5	1494	7	US-11-649-663A-2090	Sequence 2090, Ap
693	79.5	2.5	1470	6	US-10-438-246-18933	Sequence 18933, A	766	78.5	2.5	1568	6	US-10-438-246-18753	Sequence 18753, A
694	79.5	2.5	1477	6	US-10-438-246-19486	Sequence 19486, A	767	78.5	2.5	1628	6	US-10-438-246-25822	Sequence 25822, A
695	79.5	2.5	1708	6	US-10-438-246-20828	Sequence 20828, A	768	78.5	2.5	1654	6	US-10-438-246-18811	Sequence 18811, A
696	79.5	2.5	1777	6	US-10-438-246-18752	Sequence 18752, A	769	78.5	2.5	1697	6	US-10-438-246-10581	Sequence 10581, A
697	79.5	2.5	1779	6	US-10-438-246-18732	Sequence 18732, A	770	78.5	2.5	1705	6	US-10-438-246-18775	Sequence 18775, A
698	79.5	2.5	1779	6	US-10-438-246-18732	Sequence 18732, A	771	78.5	2.5	1709	6	US-10-438-246-18806	Sequence 18806, A
699	79.5	2.5	1780	6	US-10-438-246-18825	Sequence 18825, A	772	78.5	2.5	1709	6	US-10-438-246-20426	Sequence 20426, A
700	79.5	2.5	1801	6	US-10-438-246-25793	Sequence 25793, A	773	78.5	2.5	1852	6	US-10-438-246-26187	Sequence 26187, A
701	79	2.5	235	7	US-11-696-301-30	Sequence 30, Appli	774	78	2.5	1852	7	US-10-438-246-26187	Sequence 26187, A
702	79	2.5	286	6	US-10-438-246-16052	Sequence 16052, A	775	78	2.5	205	7	US-11-649-663A-4346	Sequence 4346, Ap
703	79	2.5	405	7	US-11-649-663A-3268	Sequence 3268, Ap	776	78	2.5	225	6	US-10-438-246-5831	Sequence 5831, Ap
704	79	2.5	409	6	US-10-438-246-23705	Sequence 23705, A	777	78	2.5	235	6	US-10-438-246-10823	Sequence 10823, A
705	79	2.5	412	6	US-10-438-246-16879	Sequence 16879, A	778	78	2.5	254	6	US-10-438-246-9681	Sequence 9681, Ap
706	79	2.5	412	6	US-10-438-246-24387	Sequence 24387, A	778	78	2.5	258	7	US-11-649-663A-3306	Sequence 3306, Ap
707	79	2.5	471	6	US-10-438-246-33378	Sequence 33378, A	779	78	2.5	302	6	US-10-597-034-8	Sequence 8, Appli
708	79	2.5	485	7	US-11-649-663A-3070	Sequence 3070, Ap	780	78	2.5	317	6	US-10-438-246-16829	Sequence 16829, A
709	79	2.5	486	6	US-10-438-246-20006	Sequence 20006, A	781	78	2.5	317	6	US-10-438-246-24310	Sequence 24310, A
710	79	2.5	491	6	US-10-438-246-10598	Sequence 10598, A	782	78	2.5	353	6	US-10-438-246-8305	Sequence 8305, Ap
711	79	2.5	515	6	US-10-438-246-6421	Sequence 6421, Ap	783	78	2.5	362	7	US-11-649-663A-4204	Sequence 4204, Ap
712	79	2.5	633	6	US-10-438-246-18203	Sequence 18203, A	784	78	2.5	374	6	US-10-438-246-31463	Sequence 31463, A
713	79	2.5	636	6	US-10-438-246-25293	Sequence 25293, A	785	78	2.5	422	6	US-10-438-246-33377	Sequence 33377, A
714	79	2.5	723	7	US-11-342-364-2	Sequence 2, Appli	786	78	2.5	590	6	US-10-438-246-26155	Sequence 26155, A
715	79	2.5	816	6	US-10-533-069-2088	Sequence 2088, Ap	787	78	2.5	607	6	US-10-438-246-17665	Sequence 17665, A
716	79	2.5	859	6	US-10-438-246-26065	Sequence 26065, A	788	78	2.5	651	6	US-10-438-246-18225	Sequence 18225, A
717	79	2.5	912	6	US-10-438-246-17857	Sequence 17857, A	789	78	2.5	651	6	US-10-438-246-25310	Sequence 25310, A
718	79	2.5	997	7	US-11-649-663A-4404	Sequence 4404, Ap	790	78	2.5	777	6	US-10-438-246-24385	Sequence 24385, A
719	79	2.5	1010	7	US-11-342-364-4	Sequence 4, Appli	791	78	2.5	900	6	US-10-438-246-19096	Sequence 19096, A
720	79	2.5	1019	6	US-10-438-246-18976	Sequence 18976, A	792	78	2.5	994	6	US-10-438-246-25922	Sequence 25922, A
721	79	2.5	1080	6	US-10-438-246-5628	Sequence 5628, A	793	78	2.5	1027	6	US-10-438-246-17070	Sequence 17070, A
722	79	2.5	1333	7	US-11-649-663A-1404	Sequence 1404, Ap	794	78	2.5	1262	6	US-10-438-246-20549	Sequence 20549, A
723	79	2.5	1349	7	US-11-071-761-102	Sequence 102, App	795	78	2.5	1370	6	US-10-438-246-19377	Sequence 19377, A
724	79	2.5	1370	6	US-10-438-246-10385	Sequence 10385, A	796	78	2.5	1391	6	US-10-438-246-26017	Sequence 26017, A
725	79	2.5	1545	6	US-10-438-246-20411	Sequence 20411, A	797	78	2.5	1493	6	US-10-438-246-18916	Sequence 18916, A
726	79	2.5	1596	6	US-10-438-246-19789	Sequence 19789, A	798	78	2.5	1655	6	US-10-438-246-20152	Sequence 20152, A
727	79	2.5	1596	6	US-10-438-246-26305	Sequence 26305, A	799	78	2.5	1687	6	US-10-438-246-20151	Sequence 20151, A
728	79	2.5	1635	6	US-10-438-246-18870	Sequence 18870, A	800	78	2.5	1725	6	US-10-438-246-20077	Sequence 20077, A
729	79	2.5	1640	6	US-10-438-246-20405	Sequence 20405, A	801	78	2.5	1734	6	US-10-438-246-20086	Sequence 20086, A
730	79	2.5	1687	6	US-10-438-246-20048	Sequence 20048, A	802	78	2.5	1742	6	US-10-438-246-20041	Sequence 20041, A
731	79	2.5	1708	6	US-10-438-246-20137	Sequence 20137, A	803	78	2.5	1757	6	US-10-438-246-20131	Sequence 20131, A
732	79	2.5	1735	6	US-10-438-246-20079	Sequence 20079, A	804	78	2.5	1775	6	US-10-438-246-25644	Sequence 25644, A
733	79	2.5	1792	6	US-10-438-246-20445	Sequence 20445, A	805	78	2.5	1822	6	US-10-438-246-20676	Sequence 20676, A
734	79	2.5	1792	6	US-10-438-246-20445	Sequence 20445, A	806	78	2.5	1851	6	US-10-438-246-19721	Sequence 19721, A
735	79	2.5	1819	6	US-10-438-246-18765	Sequence 18765, A	807	78	2.5	1851	6	US-10-438-246-20419	Sequence 20419, A
736	79	2.5	1843	6	US-10-438-246-25682	Sequence 25682, A	808	78	2.5	1851	6	US-10-438-246-26170	Sequence 26170, A
737	79	2.5	1851	6	US-10-438-246-20390	Sequence 20390, A	809	78	2.5	1858	6	US-10-438-246-20144	Sequence 20144, A
738	79	2.5	1851	6	US-10-438-246-26168	Sequence 26168, A	810	78	2.5	2038	6	US-10-438-246-20150	Sequence 20150, A
739	79	2.5	1897	7	US-11-649-663A-2884	Sequence 2884, Ap	811	78	2.5	2038	6	US-10-438-246-25674	Sequence 25674, A
740	79	2.5	2316	6	US-10-438-246-20067	Sequence 20067, A	812	77.5	2.5	236	6	US-10-438-246-16123	Sequence 16123, A
741	79	2.5	2433	7	US-11-649-663A-1722	Sequence 1722, Ap	813	77.5	2.5	239	6	US-10-438-246-7961	Sequence 7961, Ap
742	78.5	2.5	268	6	US-10-438-246-31969	Sequence 31969, A	814	77.5	2.5	239	6	US-10-438-246-24723	Sequence 24723, A
743	78.5	2.5	290	7	US-11-649-663A-2934	Sequence 2934, Ap	815	77.5	2.5	346	6	US-10-438-246-17336	Sequence 17336, A
744	78.5	2.5	298	6	US-10-438-246-9121	Sequence 9121, Ap	816	77.5	2.5	350	6	US-10-438-246-17541	Sequence 17541, A
745	78.5	2.5	319	6	US-10-438-246-8433	Sequence 8433, Ap	817	77.5	2.5	350	6	US-10-438-246-24679	Sequence 24679, A
746	78.5	2.5	420	6	US-10-438-246-5563	Sequence 5563, Ap	818	77.5	2.5	350	6	US-10-438-246-24763	Sequence 24763, A
747	78.5	2.5	480	6	US-10-533-069-2351	Sequence 2351, Ap	819	77.5	2.5	360	6	US-10-533-069-1074	Sequence 1074, Ap
748	78.5	2.5	529	7	US-11-649-663A-4326	Sequence 4326, Ap	820	77.5	2.5	371	6	US-10-438-246-16632	Sequence 16632, A
749	78.5	2.5	552	6	US-10-438-246-32718	Sequence 32718, A	821	77.5	2.5	371	6	US-10-438-246-24087	Sequence 24087, A
750	78.5	2.5	569	6	US-10-438-246-24522	Sequence 24522, A	822	77.5	2.5	393	7	US-11-551-744-246	Sequence 247, App
751	78.5	2.5	683	6	US-10-438-246-18246	Sequence 18246, A	823	77.5	2.5	393	7	US-11-551-744-247	Sequence 247, App
752	78.5	2.5	763	6	US-10-533-069-414	Sequence 414, App	824	77.5	2.5	417	6	US-10-438-246-33026	Sequence 33026, A
753	78.5	2.5	807	7	US-11-691-348-5	Sequence 5, Appli	825	77.5	2.5	419	7	US-11-551-744-245	Sequence 245, App
754	78.5	2.5	873	6	US-10-438-246-26044	Sequence 26044, A	826	77.5	2.5	491	7	US-11-649-663A-4442	Sequence 4442, Ap
755	78.5	2.5	1100	6	US-10-438-246-19915	Sequence 19915, A	827	77.5	2.5	497	7	US-11-215-616A-38	Sequence 38, Appli
756	78.5	2.5	1132	7	US-11-691-348-2	Sequence 2, Appli	828	77.5	2.5	514	6	US-10-438-246-25496	Sequence 25496, A
							829	77.5	2.5	529	6	US-10-533-069-599	Sequence 599, App



830	77.5	2.5	1283	6	US-10-438-246-18805	Sequence 18805, A	903	76.5	2.4	393	6	US-10-438-246-23967	Sequence 23967, A
831	77.5	2.5	1310	7	US-11-649-663A-3450	Sequence 3450, Ap	904	76.5	2.4	431	7	US-11-657-070-2	Sequence 2, Appli
832	77.5	2.5	1409	6	US-10-438-246-20192	Sequence 20192, A	905	76.5	2.4	493	7	US-11-649-663A-3528	Sequence 3528, Ap
833	77.5	2.5	1427	6	US-10-438-246-20188	Sequence 20188, A	906	76.5	2.4	513	6	US-10-438-246-25392	Sequence 25392, A
834	77.5	2.5	1441	6	US-10-438-246-20194	Sequence 20194, A	907	76.5	2.4	543	6	US-10-438-246-17537	Sequence 17537, A
835	77.5	2.5	1586	6	US-10-438-246-20179	Sequence 20179, A	908	76.5	2.4	706	7	US-11-561-363-132	Sequence 132, App
836	77.5	2.5	1587	6	US-10-438-246-26120	Sequence 26120, A	909	76.5	2.4	1328	6	US-10-533-069-1854	Sequence 1854, Ap
837	77.5	2.5	1601	6	US-10-438-246-20175	Sequence 20175, A	910	76.5	2.4	1429	6	US-10-438-246-10600	Sequence 10600, A
838	77.5	2.5	1601	6	US-10-438-246-20182	Sequence 20182, A	911	76.5	2.4	1450	6	US-10-438-246-20275	Sequence 20275, A
839	77.5	2.5	1601	6	US-10-438-246-20183	Sequence 20183, A	912	76.5	2.4	1450	6	US-10-438-246-25710	Sequence 25710, A
840	77.5	2.5	1601	6	US-10-438-246-20186	Sequence 20186, A	913	76.5	2.4	1528	6	US-10-438-246-18932	Sequence 18932, A
841	77.5	2.5	1601	6	US-10-438-246-20191	Sequence 20191, A	914	76.5	2.4	1530	7	US-11-649-663A-1862	Sequence 1862, Ap
842	77.5	2.5	1607	6	US-10-438-246-19821	Sequence 19821, A	915	76.5	2.4	1737	6	US-10-438-246-19699	Sequence 19699, A
843	77.5	2.5	1607	6	US-10-438-246-19860	Sequence 19860, A	916	76.5	2.4	1753	6	US-10-438-246-19234	Sequence 19234, A
844	77.5	2.5	1609	6	US-10-438-246-26073	Sequence 26073, A	917	76.5	2.4	1773	6	US-10-438-246-18778	Sequence 18778, A
845	77.5	2.5	1618	6	US-10-438-246-19769	Sequence 19769, A	918	76.5	2.4	1776	6	US-10-438-246-20399	Sequence 20399, A
846	77.5	2.5	1628	6	US-10-438-246-18833	Sequence 18833, A	919	76.5	2.4	1777	6	US-10-438-246-25806	Sequence 25806, A
847	77.5	2.5	1635	6	US-10-438-246-18818	Sequence 18818, A	920	76.5	2.4	1804	6	US-10-438-246-19697	Sequence 19697, A
848	77.5	2.5	1636	6	US-10-438-246-25792	Sequence 25792, A	921	76.5	2.4	1821	7	US-11-649-663A-2108	Sequence 2108, Ap
849	77.5	2.5	1685	6	US-10-438-246-20429	Sequence 20429, A	922	76.5	2.4	1929	6	US-10-438-246-9938	Sequence 9938, Ap
850	77.5	2.5	1717	6	US-10-438-246-18798	Sequence 18798, A	923	76.5	2.4	1995	7	US-11-649-663A-5544	Sequence 5544, Ap
851	77.5	2.5	1744	7	US-11-649-663A-2750	Sequence 2750, Ap	924	76.5	2.4	3229	6	US-10-438-246-10682	Sequence 10682, A
852	77.5	2.5	1750	6	US-10-438-246-19472	Sequence 19472, A	925	76	2.4	51	6	US-10-567-764-2	Sequence 2, Appli
853	77.5	2.5	1756	6	US-10-438-246-26122	Sequence 26122, A	926	76	2.4	51	6	US-10-567-764-9	Sequence 9, Appli
854	77.5	2.5	1774	6	US-10-438-246-17666	Sequence 17666, A	927	76	2.4	153	7	US-11-691-348-296	Sequence 296, App
855	77.5	2.5	1774	6	US-10-438-246-24882	Sequence 24882, A	928	76	2.4	269	6	US-10-438-246-24747	Sequence 24747, A
856	77.5	2.5	1777	6	US-10-438-246-18812	Sequence 18812, A	929	76	2.4	282	6	US-10-438-246-24099	Sequence 24099, A
857	77.5	2.5	1777	6	US-10-438-246-25807	Sequence 25807, A	930	76	2.4	328	6	US-10-438-246-16177	Sequence 16177, A
858	77.5	2.5	1791	6	US-10-438-246-20187	Sequence 20187, A	931	76	2.4	328	6	US-10-438-246-23783	Sequence 23783, A
859	77.5	2.5	1823	6	US-10-438-246-18785	Sequence 18785, A	932	76	2.4	356	6	US-10-438-246-6226	Sequence 6226, Ap
860	77.5	2.5	1827	6	US-10-438-246-20189	Sequence 20189, A	933	76	2.4	365	6	US-10-438-246-16641	Sequence 16641, A
861	77.5	2.5	1869	6	US-10-438-246-20434	Sequence 20434, A	934	76	2.4	378	6	US-10-438-246-6397	Sequence 6397, Ap
862	77.5	2.5	2187	6	US-10-438-246-19643	Sequence 19643, A	935	76	2.4	413	6	US-10-438-246-6428	Sequence 6428, Ap
863	77.5	2.5	2225	6	US-10-438-246-18928	Sequence 18928, A	936	76	2.4	424	7	US-11-649-663A-4860	Sequence 4860, Ap
864	77	2.5	354	6	US-10-438-246-18486	Sequence 18486, A	937	76	2.4	451	6	US-10-438-246-32944	Sequence 32944, A
865	77	2.5	446	7	US-11-649-663A-4744	Sequence 4744, Ap	938	76	2.4	467	6	US-10-438-246-20026	Sequence 20026, A
866	77	2.5	495	6	US-10-533-069-1589	Sequence 1589, Ap	939	76	2.4	605	6	US-10-438-246-17549	Sequence 17549, A
867	77	2.5	579	6	US-10-438-246-15816	Sequence 15816, A	940	76	2.4	620	6	US-10-438-246-23903	Sequence 23903, A
868	77	2.5	597	6	US-10-438-246-20545	Sequence 20545, A	941	76	2.4	638	6	US-10-438-246-19778	Sequence 19778, A
869	77	2.5	601	6	US-10-438-246-23578	Sequence 23578, A	942	76	2.4	769	6	US-10-438-246-18601	Sequence 18601, A
870	77	2.5	605	7	US-11-649-663A-3416	Sequence 3416, Ap	943	76	2.4	787	6	US-10-438-246-20220	Sequence 20220, A
871	77	2.5	667	7	US-11-673-094-24	Sequence 24, Appl	944	76	2.4	1004	6	US-10-438-246-17415	Sequence 17415, A
872	77	2.5	692	7	US-11-673-094-2	Sequence 2, Appli	945	76	2.4	1081	6	US-10-438-246-23550	Sequence 23550, A
873	77	2.5	707	7	US-11-673-094-68	Sequence 68, Appl	946	76	2.4	1161	7	US-11-649-663A-72	Sequence 72, Appl
874	77	2.5	826	6	US-10-438-246-18388	Sequence 18388, A	947	76	2.4	1233	7	US-11-649-663A-1468	Sequence 1468, Ap
875	77	2.5	854	6	US-10-438-246-19025	Sequence 19025, A	948	76	2.4	1333	7	US-11-657-313-23	Sequence 23, Appl
876	77	2.5	1058	6	US-10-438-246-15571	Sequence 16571, A	949	76	2.4	1501	7	US-11-649-663A-1648	Sequence 1648, Ap
877	77	2.5	1058	6	US-10-438-246-24065	Sequence 24065, A	950	76	2.4	1537	7	US-11-649-663A-2736	Sequence 2736, Ap
878	77	2.5	1199	6	US-10-438-246-20404	Sequence 20404, A	951	76	2.4	1540	6	US-10-438-246-20560	Sequence 20560, A
879	77	2.5	1199	6	US-10-438-246-26161	Sequence 26161, A	952	76	2.4	1571	6	US-10-438-246-18724	Sequence 18724, A
880	77	2.5	1283	6	US-10-438-246-20126	Sequence 20126, A	953	76	2.4	1571	6	US-10-438-246-25791	Sequence 25791, A
881	77	2.5	1283	6	US-10-438-246-25643	Sequence 25643, A	954	76	2.4	1803	6	US-10-438-246-19168	Sequence 19168, A
882	77	2.5	1298	6	US-10-438-246-20057	Sequence 20057, A	955	75.5	2.4	171	6	US-10-438-246-9546	Sequence 9546, Ap
883	77	2.5	1405	7	US-11-649-663A-2620	Sequence 2620, Ap	956	75.5	2.4	205	6	US-10-438-246-9716	Sequence 9716, Ap
884	77	2.5	1413	7	US-11-649-663A-20198	Sequence 2098, Ap	957	75.5	2.4	207	6	US-10-438-246-9185	Sequence 9185, Ap
885	77	2.5	1504	6	US-10-438-246-20109	Sequence 20109, A	958	75.5	2.4	304	7	US-11-725-235-188	Sequence 188, App
886	77	2.5	1533	7	US-11-649-663A-78	Sequence 78, Appl	959	75.5	2.4	317	6	US-10-438-246-9852	Sequence 9852, Ap
887	77	2.5	1555	6	US-10-438-246-26636	Sequence 26636, A	960	75.5	2.4	322	6	US-10-438-246-16474	Sequence 16474, A
888	77	2.5	1585	6	US-10-438-246-26265	Sequence 26265, A	961	75.5	2.4	345	6	US-10-438-246-17267	Sequence 17267, A
889	77	2.5	1592	6	US-10-438-246-25673	Sequence 25673, A	962	75.5	2.4	346	6	US-10-438-246-24753	Sequence 24753, A
890	77	2.5	1636	6	US-10-438-246-20071	Sequence 20071, A	963	75.5	2.4	389	7	US-11-649-663A-3700	Sequence 3700, Ap
891	77	2.5	1636	6	US-10-438-246-25668	Sequence 25668, A	964	75.5	2.4	390	6	US-10-533-069-2090	Sequence 2090, Ap
892	77	2.5	1705	6	US-10-438-246-15944	Sequence 15944, A	965	75.5	2.4	418	7	US-11-649-663A-3670	Sequence 3670, Ap
893	77	2.5	1785	6	US-10-438-246-18799	Sequence 18799, A	966	75.5	2.4	439	7	US-11-725-235-178	Sequence 178, App
894	77	2.5	2071	6	US-10-438-246-16609	Sequence 16609, A	967	75.5	2.4	449	7	US-11-649-663A-3138	Sequence 3138, Ap
895	76.5	2.4	121	7	US-11-528-927-513	Sequence 513, App	968	75.5	2.4	512	7	US-11-649-663A-3790	Sequence 3790, Ap
896	76.5	2.4	266	6	US-10-438-246-16241	Sequence 16241, A	969	75.5	2.4	542	6	US-10-438-246-18547	Sequence 18547, A
897	76.5	2.4	268	6	US-10-533-069-689	Sequence 689, App	970	75.5	2.4	554	6	US-10-438-246-20017	Sequence 20017, A
898	76.5	2.4	268	6	US-10-533-069-1354	Sequence 1354, Ap	971	75.5	2.4	601	6	US-10-533-069-384	Sequence 384, App
899	76.5	2.4	300	6	US-10-438-246-25523	Sequence 25523, A	972	75.5	2.4	601	6	US-10-438-246-19392	Sequence 19392, A
900	76.5	2.4	335	6	US-10-438-246-18354	Sequence 18354, A	973	75.5	2.4	603	6	US-10-438-246-17801	Sequence 17801, A
901	76.5	2.4	343	6	US-10-438-246-33207	Sequence 33207, A	974	75.5	2.4	603	6	US-10-438-246-25023	Sequence 25023, A
902	76.5	2.4	356	7	US-11-649-663A-4294	Sequence 4294, Ap	975	75.5	2.4	676	6	US-10-438-246-9874	Sequence 9874, Ap



976	75.5	2.4	749	6	US-10-438-246-15891	Sequence 15891, A	1049	74.5	2.4	1292	6	US-10-438-246-20634	Sequence 20634, A
977	75.5	2.4	749	6	US-10-438-246-23595	Sequence 23595, A	1050	74.5	2.4	1316	6	US-10-438-246-20134	Sequence 20134, A
978	75.5	2.4	1247	6	US-10-438-246-20190	Sequence 20190, A	1051	74.5	2.4	1436	6	US-10-438-246-25957	Sequence 25957, A
979	75.5	2.4	1303	7	US-11-649-663A-1570	Sequence 1570, Ap	1052	74.5	2.4	1459	7	US-10-438-246-20631	Sequence 20631, A
980	75.5	2.4	1351	6	US-10-438-246-20637	Sequence 20637, A	1053	74.5	2.4	1478	7	US-11-649-663A-710	Sequence 710, App
981	75.5	2.4	1401	7	US-11-649-663A-1338	Sequence 1338, Ap	1054	74.5	2.4	1655	6	US-10-438-246-25931	Sequence 25931, A
982	75.5	2.4	1480	6	US-10-438-246-10603	Sequence 10603, A	1055	74.5	2.4	1672	6	US-10-438-246-18808	Sequence 18808, A
983	75.5	2.4	1536	6	US-10-438-246-18791	Sequence 18791, A	1056	74.5	2.4	1672	6	US-10-438-246-18808	Sequence 18808, A
984	75.5	2.4	1578	6	US-10-438-246-20105	Sequence 20105, A	1057	74.5	2.4	1676	6	US-10-438-246-18800	Sequence 18800, A
985	75.5	2.4	1704	6	US-10-438-246-18826	Sequence 18826, A	1058	74.5	2.4	1731	6	US-10-438-246-18913	Sequence 18913, A
986	75.5	2.4	1714	6	US-10-438-246-18779	Sequence 18779, A	1059	74.5	2.4	1731	6	US-10-438-246-25952	Sequence 25952, A
987	75.5	2.4	1726	6	US-10-438-246-25825	Sequence 25825, A	1060	74.5	2.4	1731	7	US-11-649-663A-4838	Sequence 4838, Ap
988	75.5	2.4	1739	6	US-10-438-246-19251	Sequence 19251, A	1061	74.5	2.4	221	6	US-10-438-246-9440	Sequence 9440, Ap
989	75.5	2.4	2000	6	US-10-533-069-409	Sequence 409, App	1062	74.5	2.4	255	6	US-10-438-246-17718	Sequence 17718, A
990	75.5	2.4	2333	6	US-10-438-246-20193	Sequence 20193, A	1063	74.5	2.4	308	6	US-10-438-246-9287	Sequence 9287, Ap
991	75.5	2.4	3350	6	US-10-438-246-18793	Sequence 18793, A	1064	74.5	2.4	339	6	US-10-438-246-25508	Sequence 25508, A
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993	75	2.4	165	6	US-10-565-626-7	Sequence 7, Appli	1066	74.5	2.4	368	7	US-11-649-663A-2924	Sequence 2924, Ap
994	75	2.4	199	6	US-10-565-626-3	Sequence 3, Appli	1067	74.5	2.4	388	7	US-11-649-663A-3434	Sequence 3434, Ap
995	75	2.4	238	6	US-10-438-246-18455	Sequence 18455, A	1068	74.5	2.4	393	7	US-11-649-663A-4332	Sequence 4332, Ap
996	75	2.4	291	6	US-10-438-246-5856	Sequence 5856, Ap	1069	74.5	2.4	421	6	US-10-438-246-17556	Sequence 17556, A
997	75	2.4	301	6	US-10-438-246-31654	Sequence 31654, A	1070	74.5	2.4	421	6	US-10-438-246-24943	Sequence 24943, A
998	75	2.4	315	7	US-11-649-663A-3276	Sequence 3276, Ap	1071	74.5	2.4	465	7	US-11-649-663A-4168	Sequence 4168, Ap
999	75	2.4	402	6	US-10-438-246-16116	Sequence 16116, A	1072	74.5	2.4	511	6	US-10-438-246-17421	Sequence 17421, A
1000	75	2.4	408	6	US-10-438-246-9897	Sequence 9897, Ap	1073	74.5	2.4	511	6	US-10-438-246-24736	Sequence 24736, A
1001	75	2.4	428	6	US-10-438-246-6237	Sequence 6237, Ap	1074	74.5	2.4	512	7	US-11-226-240-4	Sequence 4, Appli
1002	75	2.4	444	6	US-10-438-246-18595	Sequence 18595, A	1075	74.5	2.4	518	6	US-10-438-246-18024	Sequence 18024, A
1003	75	2.4	449	6	US-10-438-246-6037	Sequence 6037, Ap	1076	74.5	2.4	542	6	US-10-438-246-19255	Sequence 19255, A
1004	75	2.4	506	7	US-11-649-663A-4286	Sequence 4286, Ap	1077	74.5	2.4	574	6	US-10-438-246-19844	Sequence 19844, A
1005	75	2.4	556	6	US-10-438-246-20488	Sequence 20488, A	1078	74.5	2.4	631	6	US-10-533-069-843	Sequence 843, App
1006	75	2.4	771	7	US-11-246-765A-77	Sequence 77, Appl	1079	74.5	2.4	631	6	US-10-533-069-845	Sequence 845, App
1007	75	2.4	776	6	US-10-438-246-16877	Sequence 16877, A	1080	74.5	2.4	707	6	US-10-438-246-25238	Sequence 25238, A
1008	75	2.4	783	6	US-10-533-069-536	Sequence 536, App	1081	74.5	2.4	778	6	US-10-438-246-20548	Sequence 20548, A
1009	75	2.4	944	6	US-10-438-246-17223	Sequence 17223, A	1082	74.5	2.4	852	6	US-10-438-246-20416	Sequence 20416, A
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1011	75	2.4	1177	6	US-10-438-246-20587	Sequence 20587, A	1084	74.5	2.4	1018	6	US-10-438-246-20578	Sequence 20578, A
1012	75	2.4	1264	6	US-10-438-246-20606	Sequence 20606, A	1085	74.5	2.4	1083	6	US-10-438-246-20546	Sequence 20546, A
1013	75	2.4	1264	6	US-10-438-246-25746	Sequence 25746, A	1086	74.5	2.4	1121	6	US-10-438-246-16950	Sequence 16950, A
1014	75	2.4	1267	6	US-10-438-246-20036	Sequence 20036, A	1087	74.5	2.4	1227	6	US-10-438-246-16988	Sequence 16988, A
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1016	75	2.4	1512	6	US-10-438-246-9945	Sequence 9945, Ap	1089	74.5	2.4	1370	6	US-10-438-246-19385	Sequence 19385, A
1017	75	2.4	1708	6	US-10-438-246-19118	Sequence 19118, A	1090	74.5	2.4	1401	6	US-10-438-246-19375	Sequence 19375, A
1018	75	2.4	1718	6	US-10-438-246-25819	Sequence 25819, A	1091	74.5	2.4	1405	6	US-10-438-246-19383	Sequence 19383, A
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1021	75	2.4	1785	6	US-10-438-246-25810	Sequence 25810, A	1094	74.5	2.4	1420	7	US-11-649-663A-2516	Sequence 2516, Ap
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1023	75	2.4	1985	6	US-10-533-069-44	Sequence 44, Appl	1096	74.5	2.4	1471	7	US-11-649-663A-2316	Sequence 2316, Ap
1024	75	2.4	2242	6	US-10-438-246-19219	Sequence 19219, A	1097	74.5	2.4	1479	6	US-10-438-246-19332	Sequence 19332, A
1025	75	2.4	3260	6	US-10-438-246-26070	Sequence 26070, A	1098	74.5	2.4	1549	6	US-10-438-246-18938	Sequence 18938, A
1026	74.5	2.4	315	6	US-10-438-246-16171	Sequence 16171, A	1099	74.5	2.4	1549	6	US-10-438-246-25861	Sequence 25861, A
1027	74.5	2.4	315	6	US-10-438-246-23774	Sequence 23774, A	1100	74.5	2.4	1566	7	US-11-649-663A-2208	Sequence 2208, Ap
1028	74.5	2.4	333	6	US-10-438-246-19993	Sequence 19993, A	1101	74.5	2.4	1567	6	US-10-438-246-20072	Sequence 20072, A
1029	74.5	2.4	352	6	US-10-438-246-6308	Sequence 6308, Ap	1102	74.5	2.4	1575	7	US-11-649-663A-2648	Sequence 2648, Ap
1030	74.5	2.4	362	6	US-10-438-246-31569	Sequence 31569, A	1103	74.5	2.4	1577	7	US-11-649-663A-396	Sequence 396, App
1031	74.5	2.4	367	6	US-10-438-246-17952	Sequence 17952, A	1104	74.5	2.4	1585	6	US-10-438-246-18869	Sequence 18869, A
1032	74.5	2.4	373	6	US-10-438-246-18417	Sequence 18417, A	1105	74.5	2.4	1605	7	US-11-649-663A-1556	Sequence 1556, Ap
1033	74.5	2.4	383	6	US-10-438-246-31840	Sequence 31840, A	1106	74.5	2.4	1689	6	US-10-438-246-20407	Sequence 20407, A
1034	74.5	2.4	386	6	US-10-438-246-9728	Sequence 9728, Ap	1107	74.5	2.4	1761	6	US-10-438-246-20432	Sequence 20432, A
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1038	74.5	2.4	426	6	US-10-438-246-6451	Sequence 6451, Ap	1111	74.5	2.4	1819	6	US-10-438-246-18746	Sequence 18776, A
1039	74.5	2.4	526	6	US-10-533-069-2156	Sequence 2156, Ap	1112	74.5	2.4	1819	6	US-10-438-246-25802	Sequence 25802, A
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1041	74.5	2.4	663	6	US-10-438-246-18985	Sequence 18985, A	1114	74.5	2.4	2458	7	US-11-649-663A-1494	Sequence 1494, Ap
1042	74.5	2.4	781	7	US-11-234-694-98	Sequence 98, Appl	1115	74.5	2.4	2659	7	US-11-649-663A-2352	Sequence 2352, Ap
1043	74.5	2.4	894	7	US-11-215-636A-36	Sequence 36, Appl	1116	73.5	2.3	278	6	US-10-438-246-9395	Sequence 9396, Ap
1044	74.5	2.4	1009	6	US-10-438-246-19094	Sequence 19094, A	1117	73.5	2.3	322	6	US-10-438-246-16473	Sequence 16473, A
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1046	74.5	2.4	1142	6	US-10-438-246-18803	Sequence 18803, A	1119	73.5	2.3	329	6	US-10-438-246-30803	Sequence 30803, A
1047	74.5	2.4	1219	6	US-11-649-663A-1462	Sequence 1462, Ap	1120	73.5	2.3	340	6	US-10-438-246-23789	Sequence 23789, A
1048	74.5	2.4	1232	7	US-11-649-663A-2840	Sequence 2840, Ap	1121	73.5	2.3	363	6	US-10-438-246-24041	Sequence 24041, A

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1123	73.5	2.3	383	6	US-10-438-246-7907	Sequence 7907, Ap	1196	73	2.3	1168	6	US-10-438-246-20632	Sequence 20632, A
1124	73.5	2.3	385	6	US-10-438-246-8432	Sequence 8432, Ap	1197	73	2.3	1217	73	US-10-438-246-19365	Sequence 19365, A
1125	73.5	2.3	423	7	US-11-551-744-196	Sequence 196, App	1198	73	2.3	1310	6	US-10-438-246-19390	Sequence 19390, A
1126	73.5	2.3	438	6	US-10-438-246-32294	Sequence 32294, A	1199	73	2.3	1340	6	US-10-438-246-26018	Sequence 26018, A
1127	73.5	2.3	442	6	US-10-438-246-24045	Sequence 24045, A	1200	73	2.3	1388	6	US-10-438-246-19360	Sequence 19360, A
1128	73.5	2.3	443	7	US-11-351-522A-34	Sequence 34, Appl	1201	73	2.3	1393	6	US-10-438-246-19287	Sequence 19287, A
1129	73.5	2.3	457	7	US-11-551-744-195	Sequence 195, App	1202	73	2.3	1393	6	US-10-438-246-19674	Sequence 19674, A
1130	73.5	2.3	482	7	US-11-607-348A-53	Sequence 53, Appl	1203	73	2.3	1393	6	US-10-438-246-19363	Sequence 19363, A
1131	73.5	2.3	487	7	US-11-698-310-8	Sequence 8, Appl	1204	73	2.3	1395	6	US-10-438-246-19364	Sequence 19364, A
1132	73.5	2.3	482	7	US-11-698-310-40	Sequence 40, Appl	1205	73	2.3	1395	6	US-10-438-246-26012	Sequence 26012, A
1133	73.5	2.3	519	6	US-10-438-246-17426	Sequence 17426, A	1206	73	2.3	1401	6	US-10-438-246-19374	Sequence 19374, A
1134	73.5	2.3	541	6	US-10-438-246-23958	Sequence 23958, A	1207	73	2.3	1401	6	US-10-438-246-19382	Sequence 19382, A
1135	73.5	2.3	553	6	US-10-438-246-23958	Sequence 116, App	1208	73	2.3	1401	6	US-10-438-246-19384	Sequence 19384, A
1136	73.5	2.3	565	6	US-11-725-235-116	Sequence 18038, A	1209	73	2.3	1405	6	US-10-438-246-19372	Sequence 19372, A
1137	73.5	2.3	565	6	US-10-438-246-18038	Sequence 25200, A	1210	73	2.3	1407	6	US-10-438-246-19379	Sequence 19379, A
1138	73.5	2.3	626	7	US-10-438-246-25200	Sequence 8, Appl	1211	73	2.3	1407	6	US-10-438-246-26016	Sequence 26016, A
1139	73.5	2.3	626	7	US-11-351-522A-8	Sequence 8, Appl	1212	73	2.3	1463	7	US-11-649-663A-1308	Sequence 1308, Ap
1140	73.5	2.3	637	7	US-11-351-522A-30	Sequence 30, Appl	1212	73	2.3	1479	6	US-10-438-246-26019	Sequence 26019, A
1141	73.5	2.3	637	7	US-11-351-522A-32	Sequence 32, Appl	1213	73	2.3	1479	6	US-10-438-246-26019	Sequence 26019, A
1142	73.5	2.3	850	6	US-10-438-246-5974	Sequence 5974, Ap	1214	73	2.3	1484	6	US-10-438-246-26260	Sequence 26260, A
1143	73.5	2.3	1011	6	US-10-438-246-18768	Sequence 18768, A	1215	73	2.3	1506	7	US-11-649-663A-1992	Sequence 1992, Ap
1144	73.5	2.3	1081	6	US-10-533-069-1214	Sequence 1214, Ap	1216	73	2.3	1547	6	US-10-438-246-26035	Sequence 26035, A
1145	73.5	2.3	1096	6	US-10-438-246-24928	Sequence 24928, A	1217	73	2.3	1547	6	US-10-438-246-26035	Sequence 26035, A
1146	73.5	2.3	1132	6	US-10-438-246-15942	Sequence 15942, A	1218	73	2.3	1600	6	US-10-438-246-26262	Sequence 26262, A
1147	73.5	2.3	1132	6	US-10-438-246-23631	Sequence 23631, A	1219	73	2.3	1600	6	US-10-438-246-26262	Sequence 26262, A
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1149	73.5	2.3	1304	7	US-10-438-246-19452	Sequence 19452, A	1221	73	2.3	1632	7	US-11-649-663A-3990	Sequence 3990, Ap
1150	73.5	2.3	1305	7	US-11-649-663A-2586	Sequence 2586, Ap	1222	73	2.3	1651	6	US-10-438-246-25984	Sequence 25984, A
1151	73.5	2.3	1329	7	US-11-649-663A-2140	Sequence 2140, Ap	1223	73	2.3	1708	6	US-10-438-246-20588	Sequence 20588, A
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1153	73.5	2.3	1421	6	US-10-438-246-18923	Sequence 2, Appl	1225	73	2.3	1716	6	US-10-438-246-26310	Sequence 26310, A
1154	73.5	2.3	1421	6	US-10-438-246-25853	Sequence 18923, A	1226	73	2.3	1724	6	US-10-438-246-18742	Sequence 18742, A
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1156	73.5	2.3	1521	7	US-11-649-663A-36	Sequence 1854, Ap	1228	73	2.3	1773	7	US-11-649-663A-1710	Sequence 1710, Ap
1157	73.5	2.3	1527	7	US-11-649-663A-1278	Sequence 36, Appl	1229	73	2.3	1795	6	US-10-438-246-19211	Sequence 19211, A
1158	73.5	2.3	1614	6	US-10-438-246-10359	Sequence 1278, Ap	1230	73	2.3	1804	6	US-10-438-246-19116	Sequence 19116, A
1159	73.5	2.3	1649	7	US-10-438-246-18782	Sequence 10359, A	1231	73	2.3	1804	6	US-10-438-246-19641	Sequence 19641, A
1160	73.5	2.3	1665	7	US-11-649-663A-1726	Sequence 18782, A	1232	73	2.3	1806	6	US-10-438-246-25900	Sequence 25900, A
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1162	73.5	2.3	1713	6	US-10-438-246-23645	Sequence 4190, Ap	1234	73	2.3	1826	6	US-10-438-246-19221	Sequence 19221, A
1163	73.5	2.3	1805	6	US-10-438-246-15228	Sequence 23645, A	1235	73	2.3	1826	6	US-10-438-246-25917	Sequence 25917, A
1164	73.5	2.3	1806	6	US-10-438-246-25826	Sequence 19228, A	1236	73	2.3	1826	6	US-10-438-246-25917	Sequence 25917, A
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1166	73	2.3	176	6	US-10-438-246-25593	Sequence 19125, A	1238	73	2.3	2499	7	US-11-649-663A-138	Sequence 138, App
1167	73	2.3	178	6	US-10-438-246-1196	Sequence 25593, A	1239	73	2.3	2534	7	US-10-438-246-20629	Sequence 20629, A
1168	73	2.3	265	7	US-11-625-795-17	Sequence 1196, Ap	1240	73	2.3	2541	7	US-11-656-389-22	Sequence 22, Appl
1169	73	2.3	282	6	US-10-438-246-31972	Sequence 17, Appl	1241	73	2.3	2605	6	US-10-438-246-26263	Sequence 26263, A
1170	73	2.3	309	6	US-10-438-246-30295	Sequence 31972, A	1242	73	2.3	2723	6	US-10-438-246-10034	Sequence 10034, A
1171	73	2.3	316	6	US-10-438-246-5860	Sequence 30295, A	1243	73	2.3	2723	6	US-10-438-246-10034	Sequence 10034, A
1172	73	2.3	360	6	US-10-438-246-31906	Sequence 5860, Ap	1244	72.5	2.3	153	7	US-11-725-235-38	Sequence 38, Appl
1173	73	2.3	382	6	US-10-438-246-20266	Sequence 31906, A	1245	72.5	2.3	191	6	US-10-438-246-8182	Sequence 8182, Ap
1174	73	2.3	387	6	US-10-438-246-16966	Sequence 20266, A	1246	72.5	2.3	193	6	US-10-438-246-8183	Sequence 8183, Ap
1175	73	2.3	387	6	US-10-438-246-24141	Sequence 16966, A	1247	72.5	2.3	266	6	US-10-438-246-16820	Sequence 16820, A
1176	73	2.3	430	6	US-10-438-246-9840	Sequence 24141, A	1248	72.5	2.3	279	6	US-10-438-246-9616	Sequence 9616, Ap
1177	73	2.3	453	6	US-10-438-246-20018	Sequence 9840, Ap	1249	72.5	2.3	335	6	US-10-438-246-25586	Sequence 25586, A
1178	73	2.3	471	7	US-11-213-575-46	Sequence 20018, A	1250	72.5	2.3	392	6	US-10-438-246-25569	Sequence 25569, A
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1181	73	2.3	548	6	US-10-438-246-24033	Sequence 16472, A	1253	72.5	2.3	444	6	US-10-438-246-16027	Sequence 16027, A
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1184	73	2.3	570	7	US-10-438-246-23887	Sequence 23887, A	1256	72.5	2.3	476	6	US-10-438-246-18618	Sequence 18618, A
1185	73	2.3	583	6	US-11-561-363-138	Sequence 138, App	1257	72.5	2.3	529	6	US-10-438-246-18540	Sequence 18540, A
1186	73	2.3	605	7	US-11-649-663A-5310	Sequence 5310, Ap	1258	72.5	2.3	536	6	US-10-438-246-19811	Sequence 19811, A
1187	73	2.3	649	6	US-10-438-246-16323	Sequence 5310, Ap	1259	72.5	2.3	622	7	US-10-533-069-2176	Sequence 2176, Ap
1188	73	2.3	680	6	US-10-438-246-30060	Sequence 16323, A	1260	72.5	2.3	666	7	US-11-249-182-52	Sequence 52, Appl
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1192	73	2.3	833	6	US-10-438-246-25889	Sequence 19522, A	1264	72.5	2.3	847	6	US-10-438-246-26154	Sequence 26154, A
1193	73	2.3	900	6	US-10-438-246-25071	Sequence 25889, A	1265	72.5	2.3	859	6	US-10-438-246-26229	Sequence 26229, A
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1270	72.5	2.3	1427	6	US-10-438-246-18930	Sequence 18930, A	1343	71.5	2.3	306	6	US-10-438-246-8483	Sequence 8483, A
1271	72.5	2.3	1427	6	US-10-438-246-18931	Sequence 18931, A	1344	71.5	2.3	360	6	US-10-438-246-8483	Sequence 8483, A
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1285	72	2.3	238	6	US-10-438-246-5848	Sequence 5848, Ap	1358	71.5	2.3	751	6	US-10-438-246-19266	Sequence 19266, A
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1333	72	2.3	1783	7	US-11-649-663A-1780	Sequence 1780, A	1406	71	2.3	606	6	US-10-438-246-26103	Sequence 26103, A
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1335	72	2.3	2314	7	US-11-649-663A-2444	Sequence 2444, Ap	1408	71	2.3	648	6	US-10-596-627-5	Sequence 5, Appl
1336	72	2.3	2555	6	US-10-438-246-10675	Sequence 10675, A	1409	71	2.3	665	7	US-11-629-727-36	Sequence 36, Appl
1337	72	2.3	2589	7	US-11-649-663A-2830	Sequence 2830, Ap	1410	71	2.3	704	6	US-10-438-246-20486	Sequence 20486, A
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1339	71.5	2.3	211	6	US-10-533-069-862	Sequence 862, Ap	1412	71	2.3	826	6	US-10-438-246-25341	Sequence 25341, A
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1435	71	2.3	1817	6	US-10-438-246-25729	Sequence 25729, A							
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1437	71	2.3	2050	6	US-10-438-246-25998	Sequence 25998, A							
1438	70.5	2.2	155	6	US-10-438-246-7579	Sequence 7579, Ap							
1439	70.5	2.2	206	6	US-10-438-246-6531	Sequence 6531, Ap							
1440	70.5	2.2	225	6	US-10-438-246-5601	Sequence 5601, Ap							
1441	70.5	2.2	231	6	US-10-438-246-24139	Sequence 24139, A							
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1443	70.5	2.2	285	6	US-10-438-246-8288	Sequence 8288, Ap							
1444	70.5	2.2	297	6	US-10-438-246-31851	Sequence 31851, A							
1445	70.5	2.2	309	6	US-10-438-246-31984	Sequence 31984, A							
1446	70.5	2.2	340	6	US-10-438-246-20047	Sequence 20047, A							
1447	70.5	2.2	355	6	US-10-438-246-18213	Sequence 18213, A							
1448	70.5	2.2	381	6	US-10-438-246-6254	Sequence 6254, Ap							
1449	70.5	2.2	387	7	US-11-649-663A-3634	Sequence 3634, Ap							
1450	70.5	2.2	391	6	US-10-438-246-19067	Sequence 19067, A							
1451	70.5	2.2	417	6	US-10-438-246-17534	Sequence 17534, A							
1452	70.5	2.2	453	6	US-10-438-246-19779	Sequence 19779, A							
1453	70.5	2.2	453	6	US-10-438-246-26294	Sequence 26294, A							
1454	70.5	2.2	484	6	US-10-438-246-17993	Sequence 17993, A							
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1456	70.5	2.2	570	6	US-10-533-069-1387	Sequence 1387, Ap							
1457	70.5	2.2	583	6	US-10-438-246-9166	Sequence 9166, Ap							
1458	70.5	2.2	583	6	US-10-438-246-9683	Sequence 9683, Ap							
1459	70.5	2.2	645	7	US-11-690-691-13	Sequence 13, Appl							
1460	70.5	2.2	654	6	US-10-438-246-31462	Sequence 31462, A							
1461	70.5	2.2	665	6	US-10-438-246-20195	Sequence 20195, A							
1462	70.5	2.2	665	6	US-10-438-246-26125	Sequence 26125, A							
1463	70.5	2.2	675	7	US-11-673-094-12	Sequence 12, Appl							
1464	70.5	2.2	705	7	US-11-673-094-11	Sequence 11, Appl							
1465	70.5	2.2	715	6	US-10-438-246-26064	Sequence 26064, A							
1466	70.5	2.2	787	6	US-10-438-246-20127	Sequence 20127, A							
1467	70.5	2.2	860	6	US-10-438-246-23836	Sequence 23836, A							
1468	70.5	2.2	910	6	US-10-533-069-1094	Sequence 1094, Ap							
1469	70.5	2.2	929	7	US-11-649-663A-3988	Sequence 3988, Ap							
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1482	70.5	2.2	1470	6	US-10-438-246-25855	Sequence 25855, A							
1483	70.5	2.2	1499	6	US-10-438-246-20501	Sequence 20501, A							
1484	70.5	2.2	1513	6	US-10-438-246-18813	Sequence 18813, A							
1485	70.5	2.2	1528	7	US-11-649-663A-4564	Sequence 4564, Ap							
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